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Direct Subminsion Submitted (24-JUN-1997) Dautenberg F.M., Molecular Neuroendocrinology, Max Planck Institute for Experimental Medicine, Rermann-Rein Street 3, 3707 Goettingen GERMANY Joostion/Qualifices

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0.94; Score 15; DB 22; Length 3477;

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Db 2335 TGGAGTAACTCAGAGGAGG 2353

Query Match 0.9%; Score 18; DB 19; Length 3349; Best Local Similarity 100.0%; Pred. No. 2.23e+01;

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QY 1224 TTCGTGTGCCTGCCTCAC 1241

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ORGANISM Mus musculus

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A From Professor (T59822) control and Hindril restriction site plus A From the Virtual State and The human G-protein barachyroid hormon (FWI) respons HINDrof (see also T59815). It respons and with a 7 primer (T39823) to amplify DNN encoding the PHF respons The PNR product was incorporated into versor poDNA)/Amp Canadiscrete Cos cells.

The Allow professor (T5982) and T59825 in the Allow product was allow product with the Allow Total Cost (T5982) and T59825 in T59825 and T59825
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       Page 25
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CRP2 receptor in host cells, in the prepn, of probes used to identify polymorphisms linked to the CRP2 receptor gove, and in the breeding of transpente animals used to study the role of the receptor in metabolism.

\*\*Required\*\*\* 1320 A.\*\* 474 C.\*\* 365 G.\*\* 355 T.\*\*

\*\*Required\*\*\* 1321 BP.\*\*

\*\*Required\*

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Query Match 1.1%; Score 23; DB 17; Length 1514; Bett Local Similarity 100(%; Pred, No. 2.446-04; Matches 23; Conservative 0; Mismatches 0; Indels 0;

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Gaps

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Query Match 0.99; Score 19; DB 29; Length 38; Best Local Similarity 100;09; Pred. Ro. 1.75e+60; Matches 18; Conservative 0; Mismatches 0; Indels

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Cotticotroni-releasing factor-2 receptor, and DNA shooding it used to isolate offer 2 receptor anasopoists for the treatment of
care declared offer 2 receptor anasopoists for the treatment of
care of 12 Rage 70.73, 109pp. Indian.
A cDNA sequence (131243) codes for at corticotropin-releasing
factor-2-alpha (GFP2-alpha) receptor (180574), a G-coupled protein
factor-1-alpha (GFP2-alpha) receptor (180574), a G-coupled protein
factor-0-alpha (GFP2-alpha) receptor (180574), a G-coupled protein
factor-0-00N. The CDNA can be used e.g. for the prodn. of recombinat
CRF2 receptor in host cells, in the prepn. of probes used or incombinat
CRF2 receptor in host cells, in the prepn. of probes used to identify
of transgenic animals used to study the role of the receptor in

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In 11244 stendard; cDNN; 1656 BP.

In 11244 stendard; cDNN; 1656 BP.

In 11244 stendard; cDNN; 1656 BP.

In 11245 stendard; cDNN; 1656 BP.

In 1245 stendard; continotrophiraleasing factor-2 receptor;

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In 2125 stendard; continotrophiraleasing factor-2 receptor;

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PR 12-28-1989; 27566.

PR 14-007-1989; 105-27566.

PR 14-007-1989; 105-27566.

PR 16-007-1989; 105-27566.

PR 16-007-1989; 105-27566.

PR 16-007-1989; 105-2766418.

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Query Match 0.8%; Score 17; DB 17; Length 20; Best Local Similarity 10.0%; Pred: No. 8.744+00; Macches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 

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standard; DNA; 28 BP.

AC 159621;
DE Ruman (-protein parthyroid hormone receptor HLTDG/4 3' PCR primer.
DE Ruman (-protein parthyroid hormone receptor; HLTDG/4; parthormone; PTH:
RW calclum: signal transduction; soonter; antagonate; hypocalcomenia;
RW calclum: signal transduction; soonter; antagonate; hypocalcomenia;
RW calclum: signal transduction; soonter; antagonate; hypophosphatemia; hypophosphatemia; hypophosphatemia; hypoparathyroidiam; chronic tetany;
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Page 31

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Page 32

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ö Query Match 08%; Score 16; DB 12; Length 35; Best Local Similarity 100(%; Pred. No. 4.078-04); Best Locales 16; Conservative 0; Mismacches 0; Indels

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PESSUT 10

20 93112 standard, DNA, 40 BP.

NO 9312 standard, DNA, 40 BP.

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NO 914091 correspond to third transmembrane domain; ss.

NO 91409 locategory transmembrane domain; ss.

NO 91409 locategory transmembrane domain; ss.

PR Secretin family; G-protein linked receptor; transmembrane domain; ss.

NO 91409 locategory transmembrane domain; ss.

PR Secretin family; G-protein linked receptor; transmembrane domain; ss.

PR Secretin family; G-protein linked receptor; transmembrane domain; ss.

PR Secretin family of transmembrane domain; ss.

PR S

Page 29

US-08-468-011A-1.rng

PEGUIZ.

D. 74473 standard: DNA: 339 BP.

D. 10-667-1939; (filter entry)

D. Manan genome fragment. G. Preferred.

N. M. detection; homology; human; adrenal tissue; ds.

D. 744-193; (and 1487)

PR. 10-704-1939; (and 1487)

PR. 10-704-1939; (and 1487)

PR. 11-704-1939; (and 1487)

PR. 11-704-19

Ouery Match Similarity 100 % Score 18; DB 10; Length 339; Best Local Similarity 100 %; Perd No. 175+00; Markens 18; Conservative 0; Mismatches 0; Indels 0;

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US-08-468-011A-1.rng

Query Match 0.8%; Score 17; DB 29; Length 28; Best Local Similarity 100.0%; Pred. No. 8.744+00. 1 Matches 17; Conservative 0; Mismacches 0; Indels 0;

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AC 077851. 10 067851 trandard: DNA; 33 SP.
AC 077851. 10 067851 trandard: DNA; 33 SP.
AC 077851. 10 067

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Page 36
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Deliver, 1997 (first entry)

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O.84; Score 16; DB 29; Length 183;
Best Local Similarity 10:04; Pred 10:04; Order 01;
Matches 16; Conservative 0; Mismatches 0; Gaps
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AC 059641 at andard: CDNA; 137 BP.

DY C 059641 and brain Experience Top EST01496.

DE Human brain Experenced Sequence Top EST01496.

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/product= Antibody light chain fragment.
/note= Probably exon.
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AC 40135: AC 4013 BP.

AC 40135: AC
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(SUMO ) SUNITONO CREM CO LI
(SUMO ) SUNITONO SZIYAKU KK
PRI, 93-2589081/44.
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PD 13-X00-1993.

PD 13-X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-468-011A-1.rng
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/label= I
misc_difference 35
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misc_difference 38
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ID T65671 standard; DNA; 183
                                                                                                                                          misc_difference 26
Tue Nov 24 08:10:57 1998
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Provided antibody and a recombinant for its produ. Includes
1 1-0-Main is matthoody being replaced by L-chain like protein contg.
2 1 1-0-Main is matthoody being replaced by L-chain like protein contg.
3 1 1-0-Main is matthoody for a serial contg.
3 1 1-0-Main is many cell HI221.
3 1 1-0-Main is many cell HI222, a HIZ22 gete library was prespected from the common synomic DNA and the Main adiabat space are percented. The common synomic DNA and the matthoody space was analysed and the hase confirmed to containing the antibody space was determined and the hase confirmation of an L-chain-like protein. The sequence of the protein of an L-chain-like protein. The sequence of the protein SS Sequence 619 BP: 124 A: 196 C; 143 G; 143 G; 156 T; 888888888333

ö Ouery Match 0.8%, Score 15; DB 8; Length 619; Met Local Similarity 100:0%, Pred. No. 4.076-01; Metchen 15; Connervative 0; Minmatches 0; Indels 0; Gaps

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g. T 15 N30131 standard; DNA; 640 BP. 

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19-Juli 1999 ((first entry)
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19-Juli 1999 ((first entry))
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FF EP-66831-A. (\*Tage a processes and the control of the control o

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The present sequence encodes the terminal portion of the coding sequence of the truncated hepsotroyte control of untransactar injury of the truncated hepsotroyte control of the truncated of the complete in cells expressing the MFPT such cells can be transplanted in the complete the truncated form the control of the complete in cells expressing the MFPT control of the useful in treating hyper-prolificative the man formal plant disorders. Both MFPT control of the useful in treating hyper-prolificative control of the useful in treating hyper-prolificative control of the useful control of the us

Ouery Match 0.8% Score 15; DB 12; Length 658; Best Local Similarity 10.0% Pred, No. 4.074-601; Machae 15; Connervative 0; Mismatches 0; Indels 0; Gaps

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ESSULT 17

10.19149 trandard; RNA: 693 BP.

10.19140 trandard; RNA: 694 BP.

10.19140 trandard; RNA

Page 39

Page 40

two different FMDV strands, and encoding DNA. Pref. the fusion polypopited has the sequence of two of the A, C, O, Aska-1, SAI 1, SAI 2, ANY 2 and SAY 3 type strains of the virus. The polypopiteds pref. comprises AMS 55-170 or 1-210 of the VPJ virus. Pushon polypopited and any comprise AMS 1-210 fused to 8-210 of VPJ virus protects. PPMJ, P

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Ouery Match 0.8%; Score 16; DB 4; Length 693; Best Local Similarity 93.8%; Pred. No. 4.074-01; Matches 15; Conservative 1; Mismatches 0; Indels Matches 15.

RESULT 18 N93120 standard; CDNN, 705 BP.

10.7017-1990 (Itart entry)

BE 13.7017-1990 (Itart entry)

BE 13.7017-1991 (Itart

Page 38

US-08-468-011A-1.rng

may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. pFM1, pFM2, pFM3, pFM3, pFM3, pFM3, pFM3, pFM2 and pFM6 are also claimed.
Sequence 640 BP; 159 A: 197 C; 158 G; 126 T;

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Query Match
Query Match
Deal Similarity 100 04, Pred. No. 4.07e+01;
Matches 16; Conservative 0; Missatches 0; Indels

RESULT 16
T79411 stndard; CDNN: 658 BP.

D 779411 stndard; CDNN: 658 BP.

T79411 stndard; CDNN: 658 BP.

T79411 stndard; CDNN: 658 BP.

T79411 stndard struct variant 2.2b RGF/RXI terminal portion CDNN.

RM GARDER STRUCT (SAIN) chancherapeutic, human; as.

LOAD LOAD STATE STRUCT (SAIN) chancherapeutic, human; as.

FT CASE STATE STATE STRUCT (SAIN) chancherapeutic, human; as.

FT FILMET DAID (SAIN) common structure of the structure structure of the structure of t

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168 G; 146 U; 693 BP; 177 A;

Ouery Match 08%; Score 17; DB 1; Length 705; Best Local Similarity 100.08; Pred. No. 9.74e-00; Matches 17; Conservative 0; Mismatches 0; Indele

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Tue Nov 24 08:10:57 1998
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US-08-468-011A-1.rng

Page 42

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Page 41

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We woosand the second and the second and the second and the second and second
                                                                                                                                                                                                                                                                                                                                                                  5'-phosphate;
NESUIT 197

TESTIF 2011 standard: DNA: 750 BP.

TESTIF 2011 standard: DNA: 750 BP.

TESTIF 2011 standard: DNA: 750 BP.

TESTIF 2012 Standard: DNA: 750 BP.

TESTIF 2014 BASE STANDARD S
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Outery Match (0.8); Score 16; DB 30; Length 750; Best Local Similarity 100:00; Pred. No. 4.078+01; Marches 16; Conservative (0. Manatches 0; Indels 0; a

PN 9912685-1.
PN 9012685-1.
PN 9012685-1.
PN 9012685-1.
PN 9012691.
PN 9012691.
PN 901291.
PN 90129

misc\_signal misc\_signal misc\_signal

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078979; dendard; DNA; 819 BP.
078979; de Abd: 1805 (fitter entry)
Human imminoglobulin variable heavy chain #41.
Primer: PCR, amplify; human immunoglobulin; variable; heavy chain; cosmid; placenta, vector; pDBA; E.coli; mammallan; ds.
key Lossido, Qualiffers
1995, 639 (malifiers

50 RESULT Tue Nov 24 08:10:57 1998

US-08-468-011A-1.rng

RESULT 11

Nalling Square conceding the property of T colubriformia.

Landing Square according the protein of T colubriformia.

Recastic neceding the protein of T colubriformia.

Squares according the protein of T colubriformia.

P Extractic neceding the protein of T colubriformia.

P 12-An-1989.

P 02-UU-1989. AU0319.

P 03-UU-1989. AU0319.

Query Watch 0.8%; Score 17; DB 1; Length 960; Best Local Similarity 100:00, Pred. No. 8.74+00; Local Similarity Conservative 0; Himmatches 0. Indels 0; Gaps ద

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0; Mismatches 0; Indels Matches 16; Conservative

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Page 43

Tue Nov 24 08:10:57 1998

Query Match 0.8%; Score 16; DB 13; Length 819; Best Local Similarity 100.0%; Pred. No. 4.07e+01;

PP 27-ADC-1994.

PR 67-ERD-1993; CA-090552.

PR 67-ERD-1993; CA-09052.

CA-09053; CA-09052.

CA-09053; CA

ö Omery Match 0.8%; Score 16; DB 12; Length 1030; Best Local Similarity 100:0%; Pred 16:0, 4.079-0; Indels 0; Caps Matches 16; Conservative 0; Mismatches 0; Indels 0; Caps 

Page 44

Page 46

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produce plants

bialophos and L-phosphinothricin. The gene may be used to with herbicide resistence equence 1200 BP: 156 A: 428 C; 416 G; 160 T; Query Match

0.8%, Score 16, DB 1; Length 1200,

Bat Local Similarity 100.0%, Pred, No. 4.078-40;

Matches 16, Conservative 0; Mismatches 0; Indels

Matches 16, Conservative 0; Mismatches 0; Indels

US-08-468-011A-1.rng

Tue Nov 24 08:10:57 1998

Page 45

PR 04-MW-1991; UG-057222.

PA (DOWE) DOWERAND M.)

A (DOWE) DOWERAND M.)

PROPER STOOTH MAYER M.)

PROPER M.)

PROPE Ouery Match

O.84, Score 16; DB 13; Length 1030;

Batch Local Similarity 100:04, Pred. No. 4.070-01;

Matches 16; Conservative 0; Mismatches 0; Gaps Cp 1756 CCACACATGCCATTC 1741 873 ccacacatgtccattc 888 a

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REBUIT 24

ID 80997 and 80990 (first entry)

ID 52-184-1990 (first entry)

ID 52-184-1990 (first entry)

ID 62-184-1990 (first entry)

ID 62-184-1990 (first entry)

REP 52-184-1990 (first entry)

REP 52-191033-A.

PH REP-331033-A.

PD 20-282-1990 (PG 52-1990 (PG 62-1990 (PG 62-1990

PF EP-131033-A.
PP 20-131033-A.
PP 20-131033-A.
PP 20-131033-A.
PP 20-131033-A.
PP 20-13103-A.
P

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US-08-468-011A-1.rng

167 C; 219 G; 417 T; CC and 9.6. SQ Sequence 1260 BP; 457 A; Query Match 0.8%; Score 16: DB 22; Length 1260; Best Local Similarity 100:0%; Pred Nov. 4.076+01; Matches 16: Conservative 0: Minmatches 0; Indels 0;

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Db 1080 atggaatttgtgggt 1095 | Cp 757 ATGGAATTTTGTGGGT 742

wolli223.4. coupled receptor'

WHO STATES AND STATES AN

Page 47

Tue Nov 24 08:10:57 1998

US-08-468-011A-1.rng

PR N0960017.A2.

PR P-PEDD: NET PAGETRE.

PR N096001.A2.

PR N096001

RESULT 12

ID 17104; standard; DNN: 1260 BP.

Or 17104; standard; DNN: 1260 BP.

Or 17104; standard; DNN: 1260 BP.

Or 17104; standard; DNN: 1260 BP.

RW Interticulate control of the con

expensive and labour intensive then previous methods and does not treated and continued to the industriant of membrane Iragments from responsive titismus or cell lines or cell lines or cell lines or cell lines are as follows: (1) the C-terminal internal effectory domain is replaced; (2) the N-terminal extracellular and C-terminal internal effector domain ser prejaced; and (3) the N-terminal Internal effector domain are replaced; and (3) the N-terminal C-terminal internal effector domain are replaced; and (3) the N-terminal C-terminal internal effector domain are replaced; all with the G-terminal of the S-terminal contrasp, domains of the S-terminal contrasp. As a second of the S-terminal C-terminal internal effector domain are replaced; all with the G-terminal contrasp. As a second of the S-terminal C-terminal C-terminal C-terminal S-terminal C-terminal S-terminal C-terminal C-t

Length 1287; Opery Match

O.84; Score 16; DB 2; Length 1287;
Best Local Similarity 100.04; Fred, Nov. 4.070-401;
Destrobes 16; Conservative 0; Mismarches 0; Indels

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PER WOO410136-A.

PD 11-MAY-1994.

PD 11-MAY-1994.

PD 11-MAY-1994.

PD 10-WOY-1992. (G.9-57158).

PR 05-WOY-1992. (G.9-57158) RESULT 17

065355 standard; DNA, 1340 BP.

065355 standard; DNA, 1340 BP.

065350 standard; DNA, 1340 BP.

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Page 48

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PF M03105159-A.

18-MAR-1933.

18-MAR-1933.

18-MAR-1933.

18-MAR-1931.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC 910464;996 (first entry)
DE P 9105419196 (first entry)
R Remanglutinin heemaglutinin gene hagA repeat RArep3.
R Remanglutinin heemaglutinin per periodontal disease; vaccine; probe;
RR PREP5; as 1000 probe; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit; probe; plant; lignin; biosynthesis; biosynthesis; cellulose; digetibility; feed coup; pshhopen; timber; ss. strongan atheorizan theory and the coup.
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0.8%; Score 17; DB 6; Length 1393;

bet Local Similarity 100:0%; Pred. No. 8.74e*0; Indels 0; Gaps Matches 17; Conservative 0; Minmatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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O.8%; Score 16; DB 21; Length 1368;
Best Local Smilarity 100.0%; Pred. No. 4.07+01;
Marches 16; Conservative 0; Mamarches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                           Query Match 1350, Best Score 17, DB 9; Length 1350, Best Local Similarity 100.0%; Perf No. 974+00. 774+06. We hatches 17; Conservative 0; Mamatches 0; Indels 0;
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/transl_except= (pos: 338..340, aa: Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT. 13.0 standard; CDNA to mRNA; 1400 BP.

7.03129 standard; CDNA to mRNA; 1400 BP.

DE 20-ARR-1998 (first entry)
DE 20-ARR-1998 (first entry)
DE 20-ARR-1998 (first entry)
DE 20-ARR-1998 (first entry)
NA mathmatic disease; ss.

NA mathmatic disease; ss.

NA mathmatic disease; ss.

OS HONO sapiens. Location/Qualifiers
PT CDS //tanal_axcept* (pos: 338..340, as: X
                                                                                                                                                                                CC overlapping subfragments.
SQ Sequence 1350 BP; 481 A; 232 C; 329 G;
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84..1155
/*tag= a
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Of 1964's atandard; DNA; 1168 BP.

DC 1964's atandard; DNA; 1168 BP.

DC 1964's atandard; DNA; 1168 BP.

DC 1964's atandard; DNA; 1168 BP.

NW ARRED; BILLINI, hapA gene; period

NW MARRED; BILLINI, hapA gene; period

NW MYSEL'S ATANDARS.

DN 11-DNE-1955's 10108.

PR 01-DNE-1955's 1010
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PD 05-37A-1994.

PD 05-3AA-1994.

PE 05-3AA-1995.

PE 05-3AA-1996.

PE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 31
1D 408027 standard: CDNs; 1393 BP.
1D 608027 standard: CDNs; 1393 BP.
DT 16-0UL-1993 (first entry)
DE CAD 6084 isolated from pTCAD14.
NW TODACCO: cinnamyl alcohol dehydrogenase; CAD; tryptic peptide; primer;
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No. 8.74=00; Indels 0; Gaps Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTEGERATE 30

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INTEGERATE AND SECRET STATE ST
       US-08-468-011A-1.rng
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
O.8; Score 16; DB 10; Length 1340;
Best Local Similarity 100.0%; Pred. No. 4.07e+01;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
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10 G54397; standard: DNA: 1150 BP.
10 G54397; standard: DNA: 1150 BP.
10 G54397; standard: DNA: 1150 BP.
10 G54397; standard: George Control Theory (G54397); standard: G64397; standa
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                                                                                                                                                                                                                                                                                    393 T;
                                                                                                                                                                                in other bacterial strains.
See also Q65354.
Sequence 1340 BP; 500 A; 185 C; 262 G;
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Page 52

Page 50

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DNA encoding mammalian cannabinoid receptor - used for producing receptor for servening drugs and lighands and in detection by the receptor for servening drugs and lighands and in detection by the bollolouser Fig. 3: 1559; English.

CC STRE CDNA encoding the Fat Cannabinoid receptor was isolated from a cart cerebral cortex CDNA library. An Ecodity Nabl fragment was used to sequenced. There is confirmed to the recent and the confirmed to the sequences of the muan and recentablicid receptors.

CC STREAM of the confirmed to the co
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                                                                                                                                                                                                          coDM, which was isolated from planning pyrolly. The GAD cDNN may be used in the production of a recombinant DNN comprisents such that is essential to plant lighth bloogynthesis when incopprated that plant spence by transformation, mRNN transcribed from the codding tregion inhibits production of the engine from the endegenous gene. The recombinant DNN may be used to provide plants having altered inguility to sprintesis a lighnin, in woody feedbrooks for callulose filter crops, reduction of lighn in woody feedbrooks for callulose filter extraction, improvement of the response of crop plants to pathogen extraction, improvement of the response of crop plants to pathogen sequence 119 page 1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.8%, Score 17, DB 6; Length 1419; Best Local Similarity 10.9%, Pred. No. 8.74e-00; Indels 0; Gaps Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps
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0.9%, Score 16; DB 3; Length 1507;
Best Local Similarity 100, Pred. No. 4.07e-01.

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps
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10 (34050 standard; CDNA to mRNA; 1560 BP.

11 (3-010-1994 (first entry)

12 (-010-1994 (first entry)

13 (-010-1994 (first entry)

14 (-010-1994 (first entry)

15 (-010-1994 (first entry)

15 (-010-1994 (first entry)

16 (-010-1994 (first entry)

17 (-010-1994 (first entry)

18 (-010-1994 (first entry)

19 (-010-1994 (fir
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No. 201001.

No. 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 0.8%; Score 1s; DB 2; Length 1499;
Best Local Similarity 100.0%; Pred. No. 4.078-01;
Macches 1s; Connervative 0; Mismatches 0; Indels 0; Gaps
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18-MR-1932; 000774,

18-MR-1933; 0007
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93..1165
/*tag* a
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10 770057; acadard; cDNA, 1603 BP.
27 20-VOG57;
Cotton (Eds. Fibre; premoter; transgenic plant; truncated;
Cotton (Eds. Fibre; premoter; transgenic plant;
Cotton (Eds. Fibre; premoter; transgenic plant;
Cotton (Eds. Fibre; plant)
Cotton (Eds. F
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             US-08-468-011A-1.rng
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Pred. No. 4.07e+01;
0; Mismatches 0; Indels 0;
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Homo sapiens. Location/qualifiers

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/togg - g primer binding site / 1111.146
/togg - g primer binding site / 1016 - 3 primer binding site
                                                                                                                                                                     0; Mismatches
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13.111
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complement (10.27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 1603 BP.
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ID T30267 standard; DNA; 1603 BP.
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Best Local Similarity 100.0%;
Matches 16; Conservative
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Sequence 1640 BP;
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Tue Nov 24 08:10:57 1998
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Page 57
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M. Course fibre: propoperity could close cirp-id.

M. Could fibre: propoperity could creening leaf; ownle; root; or could could be c
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DE COLLON (IDNE-perceific CDNA, 1604 LONE)

DE COLLON (IDNE-perceific CDNA, clone H.

COLLON (IDNE-perceific CDNA, clone H.

No Cotton (IDNE-perceific CDNA, clone H.

DE COLLON (IDNE-perceific CDNA)

NO COSSAPPLE DE COLLON (IDNE-perceific CDNA)

PR USASSADOR (IDNE-perceific CDNA)

PR USASSADOR (IDNE-perceific CDNA)

PR 12 NOV-1988; 2032334.

PR 12 NOV-1988; 2032334.

PR 12 NOV-1988; 203-203230.

PR 12 NOV-1988; 203-203230.

PR 12 NOV-1988; 203-203230.

PR 14 NOV 150-1989; 203-203230.

PR NOW 150-1989; 203-203230.

PR NOW 150-1989; 203-203230.

PR COLLON PR COLLON (17-50, 48pp; English.

PR COLLON (IDNE-RAN, 2010-8 H. (11)250) vas lackted from a CDNA IDRARY of COLLON (IDNE-PERCEIF) (IDNE-PERCEIF) (IDNE-PERCEIF)

CC COLLON (INN. Sen Island using a subtractive hybridisation procedure CC The clone hypridisation procedure CC The clone hybridisation procedure CC The collection hybridisation hybridisation procedure CC The collection hybridisation hybridisat
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O.81, Score 17, DB 10, Length 1560,

Bert Local Similarity 100, Pred. No. 8,744-00,

Matches 17, Conservative 0; Mismatches 0, Indels 0, Gaps
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US-08-468-011A-1.rng
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                                                                                                                                                                                                 Bone Commention inducting spreed in . Cor theresp of diseases involving osteoperosis, a bone deficiency such as alveolar pyorrhee etc. and bone freeture.

Protein having improved bone formetion inducting-activity forceton having improved bone formetion inducting-activity has been provided. By make the form the tissue of a verrebrate (e.g. human, rat) and used in recombinant bus useful in pharmaceutical.

Solvential in the production of the protein. The Bip is useful in the production of the protein. The Bip is a security of the protein in the security of the s
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D 115869 standard; cDNN: 1640 BP.
AC 115868.1997 (first entry)
DT 1174NX-1997 (first entry) R Musan booken exceptospate protein-10 cDNA.
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Page 60

Page 58

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16; Conservative
Matches
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US-08-468-011A-1.rng

Page 62

PESSUIT.

111134 attendenti DNN: 1869 BP.

111134 DE CC-Chemochine receptor 3 genome DNN.

111134 DE CC-Chemochine Companie DNN.

111135 DE CC-Chemochine DNN.

111135 DE COMPANIE DNN.

111135 DE COMPANIE DNN.

111135 DE COMPANIE DNN.

111135 DE COMPANIE DNN.

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11135 DNN.

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MINE AND STATES STATES AND STATES

PR W0962237-A2.

In the specification.

PD 32-VUL-1996.

PR 19-7AK-1996.

PR 19-7AK-1999.

PR M09700960-A1. /Product= cxta.

PD 09-ANA-1997.

PR 21-UTW-1995; UG 02-94059.

PR 21-UTW-1995; UG 02-94059.

PR 12-UTW-1995; UG 02-94059.

PR 12-UTW-1995;

Tue Nov 24 08:10:57 1998

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Page 64

749.1800 749.1800 74.249 b 532.1800 1801.1810 /more - 181 nucleotides of introm 2758

PER NO9111167-A.
PD 05-2EZ-1930.
PD 05-2EZ-1920.
PD 05-2EZ-1930.
PD 05-2EZ-1930.
PD 05-2EZ-1930.
PD 05-2EZ-1920.
PD 05-2EZ-1930.
PD 05-2EZ-1930.
PD 05-2EZ-1930.
PD 05-2EZ-192 RESULT 43

TO 011373 standard; DNA; 1810 BP.

DE 253 specific cons Billianer detail receptor; hormone; se.

DE 253 specific cons Billianer detail receptor; hormone; se.

DE 253 specific cons Billianer detail receptor; hormone; se.

Transcription unit; linect staroid receptor; hormone; se.

PR EXP 150 specific cons Billianer detail detai

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Query Match 0.8%; Score 16; DB 23; Length 1689; Best Local Similarity 100.0%; Pred. No. 4.07e+01;

compable of orimulating cosinophil accumulation and/or attracting conclophile (including compeasate). Binds.

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Page 63

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Query Match
O.8%; Score 16; DB 32; Length 1689;
Best Local Similarity 100:00, Pred. No. 4.070-01;
Matcheo 16; Concervative 0; Mismachone 0; Indels 0; Gaps 431 A; 416 C; 344 G; 497 T;

Ouery Match
Ouery Match
Bet Long Similarity 100.04; Pred. no. 4.076-07.
Bet Checks 16; Conservative 0; Mismarches 0; Indels

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0; Gaps

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Page 66
US-08-468-011A-1.rng
 Tue Nov 24 08:10:57 1998
Page 65
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US-08-468-011A-1.rng

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16:90R-1993 (first entry)
16:90sum Adday PH/PPTPP receptor clone, OK-O.
16:90sum Adday PH/PPTPP receptor clone, OK-O.
16:00sum Adday PH/PPTP receptor clone, OK-O.
16:00sum Adday PH/PPT

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119949: (first entry)
Oposaum Kaday PHYPPTPP receptor CDRA clone OK-H.
Oposaum Kaday PHYPPTPP receptor cDRA clone OK-H.
Parathyroid hormone: receptor: parathormone: PTH:
parathyroid hormone: parathormone: par
                                                        standard; cDNA; 1862 BP.
| 119945 | 14 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 119945 | 11994
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RESULT 45
ID Q29605 standard; cDNA; 1863 BP.
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Score 17; DB 18; Length 1862; Pred. No. 8.74e+00; 0; Mismatches 0; Indels 0; Gaps

Ouery Match Best Local Similarity 100.0%; Matches 17; Conservative

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PH 1055494806-A. Pritage a property of the pro
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Ouery Match 0.8%: Score 17; DB 18; Length 1863; Best Local Similarity 100.0%; Pred. No. 8.744-764 0. Indels 0; Gaps Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps

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19356 standard; CDNN: 1935 BP.

19356 standard; CDNN: 1935 BP.

19400 standard; CDNN: 1935 BP.

19506 standard; CDNN: 1935 BP.

19507 standard; CDNN: 1935 BP.

19508 standard; CDN
                                                                      Gaps
Query Match

Best Local of Soure 17, DB 5; Length 1861;

Best Local of Soure 17, Pred. No. 0, 7744-0, 0, 104els 0, Mismatches 0, Indels 0,
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0.84; Score 16; DB 34; Length 1915;
Best Local Similarity 100,04; Pref No. 407e-01;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
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Page 68

Page 67

US-06-468-011A-1.rng

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Tue Nov 24 08:10:57 1998

DE 02-02-1997;
PR 27-1487-1987;
PR 27-1487-1986;
PR 27-1487-1986;
PR 27-148-1986;
PR 27-148-19

Ouery Match

O.8%; Score 16; DB 38; Length 1999;

Best Local Similarity 100:04; Pred 100:4.079-01;
Matches 16; Conservative 0; Mamatches 0: Gaps

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DD 11-WAY-1989.

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PR 11-WOY-1987.285637.

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| RESULT | 48 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.00 | 100.0

REBULT 50

ID 039607 standard: CDNA; 2006 BP.

IC 40404:1993 (first entry)

DE Haman Aiday PHT/PTIEP preprofice of the matagonist;

Restablyzed hormone: related protein; calcium; antagonist;

NW antibodies: hypercalcaemia s9:

NW NW 18193: US 681703
PR 6-MR-1991: US 681705
PR 6-MR-1991: US 681775
PR 6-MR-1991: US 681775
PR 6-MR-1991: US 681775
PR 6-MR-1991: US 681775
PR 793-66271/44
NW 193-96271/44
DR 973-96271/44
PR 973-96271/

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Ocery Match (1913); Score 16; DB 1; Length 1913); Bent Loral Similarity 100:09; Pared. No. 4.00+0.1; Matches 16; Conservative 0; Mismatches 0; Ocean 16; Conservative 0; Mismatches 0.

REGOUT 49
TO 2015 Cotandard: cDNA to mRNA; 1999 BP.

A T1320 Cotandard: cDNA to mRNA; 1999 BP.

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PR M09217602-A.

13-027-1992.
PR 05-APR-1991; 002821.
PR 05-APR-1992; 00-681702.
PR 05-APR-1992; 00-681702.
PR 06-APR-1992; 00-68

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Query Match

O.8%: Score 16; DB 5; Length 2006;
Best Local Similarity 100:04; Pred No. 4:070+01;
Matchen 16; Conservative 0; Himmatchen 0; Indels 0; Gaps 0;

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THE NOW 24 0811101 1998  105 0.9 655 1 001046 D9441.6P  106 0.9 655 1 001051 SERVATE DESTRUCCENSE, 4884-01  971 5 0.9 665 4 000513 SERVATE DESTRUCCENSE, 4884-01  972 5 0.9 665 4 000513 SERVATE SERVATE SERVED SERV	PRECURS   AUGUST
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PROKARYOTA: GRACILICUTES: SCOTOBACTERIA; FACULTATIVELI ANAEROBIC RODS;
ENTEROBACTERICALE.
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NO 22181.

NO 62181.

OLUMI-1999 (TRESDIERL 06, CREATED)

DT 01-UNI-1999 (TRESDIERL 06, LAST SEQUENCE UPLATE)

OLUMI-1999 (TRESDIERL 06, LAST SEQUENCE UPLATE)

OLUMI-1999 (TRESDIERL 06, LAST SEQUENCE UPLATE)

OLUMI-1999 (TRESDIERL 06, LAST ANNOTATION UPLATE)

OC PROMANYOR, GRADILLUTTES, SCOTOBACTERIA, ARROBIC RODS AND COCCI, PROMANYOR PROMANYOR OF STRAINSOURCE FROM N.A.

RA KITTER 7. KINSCHER 7. C. MCEVOY J.L., WILLIS D.K.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Questy Match 1.3%; Score 7; DB 1; Length 164; Dast Local Similarity 100.04; Pred. No. 2.22+00; Matches 7; Conservative 0; Minmatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 1.51; Score 8: DB 9: Length 1904;
Best Local Similarity 100.08; Pred No. 1.67-00; Indels 0: Gaps
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps
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10 065023 PRELIMINARY, PRT; 125 AA.
C 065023 PRELIMINARY, PRT; 125 AA.
C 065023 CREATED. 07, CREATED.
DT 01.A0G-1998 (TREABLEL, 07, LAST SEQUENCE UPDATE)
DT 01.A0G-1998 (TREABLEL, 07, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 13.0 KD PROFIEIN.
CAN MITCOSACCIENTUM TUBERCULOSIS.
C MITCOSACCIENTUM TUBERCULOSIS.
C PROKARYOTA: FIRMICUTES, ACTINOMYCETALES, MYCOBACTERLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13% Score 7: DB 2: Length 166; Best Locots Similarity 100.0% Pred. No. 2.228-00; Mecches 7: Conservative 0; Mismatches 0; Indels Maches 10; Mismatches 0.
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DO 59370

DO 59370

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DO 5940
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SECURNCE FROM M.A.
SECURNCE PROM P. L., WILLIS D.K.;
KITER T., KINSCHERF T.G., MCEWOR J.L., WILLIS D.K.;
STBAKITERS T. A. C. 1931) TO EMBL/GENBARK/DDBJ DATA BANKS.
EMBL. APO21809: 62736141,
SEQUENCE 116 AA: 12609 MW; D881152C CRC12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURNE FROM N.A.
WRITE-CTI. 1978 S. HILL C.W.: BANK, DBJ DATA BANKS.
CHRITED C.AM-1399; TO EMB_GENBANK, DBJ DATA BANKS.
EMB. AFO4450. 12220441.
RFPOTERTICAL PROPERTY
SEQUENCE LE6 AA: 18051 PW: 79957757 CRC32;
                                                                                                                                                                                                                 APPL. ENVIRON. MICROBIOL. 3:0-0(0).
EMBL: L44593; G928828; -.
SEQUENCE 1904 AA: 204786 MM; EDA9245B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQ SEQUENCE 164 AA; 19056 MW; F78D25C6 CRC32;
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406 GFFVSII 412
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11 OSS313 PRELIMINARY: PRT: 164 AA.

OSS313 PREMEMBER. 07. CREATED)

DI 1.AGC-1988 (REMEMBER. 07. CREATED)

DI 1.AGC-1988 (REMEMBER. 07. LAST SECORDE UPDATE)

DI 1.AGC-1988 (REMEMBER. 07. LAST SECORDE UPDATE)

DI 1.AGC-1988 (REMEMBER. 07. LAST ANNOTATION UPDATE)

CAN PRINCACCUS MODITOSHII.

OC ARCHARLE THANGEMENT THERMOCOCCALES; THERMOCOCCACAE; PIROCOCCOS.

RESULTA FOOD N. AGC AND M., HORINAM H., HAIRAN Y., HINO Y., ANALANIN M., ORIVINI Y., SHALL M., NORTHIN M., ORIVINI Y., NORTHINO Y., MARCHIN Y., 
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BLIKAMA Y., HINO Y.,
INAMADOS S., SERIER H., MARA S., SOGOGI H., BOSOTAMA M., MAGA Y.,
SAKAT H., COGDA K., OTSUGA R., MARARAMA H., TAKAMITA M., OBFOGI Y.,
PUNAMASHI T., TANKA T., TANKA T., TONOSI Y., TAMARANI M., CORTHANA,
ACAT K., TOSHIGAMA T., NAKAMORA Y., MASOGI Y., SHIGHTED DOCE-1997) TO BELLOCERIAN T., MASOGIRI Y., SHIGHTER PEREL, MASOGIRI Y., SHIGHTER PEREL, SHOOGH S.,
PEREL, ABOOGH S., DELLOCERBANK, DEBG DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7

10 071768

M. O71769

D. O1769

D. D1760

D. D
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GTRAILLE N.A.; POLICE S., EIGLMEIER K., PASCOPELA L.,
PHILIPP N.J., POULE S., EIGLMEIER K., PASCOPELA L.,
PHILIPP N.J., POULE S., INCARABANINA V., MEYN B., BERCH S., BLOOM B.R., JACOBS W.R., JR.,
COLE S.T.,
COLE N.T., ACAD. SCI. U.S.A. 93:3132-3137(1996).
PROG. NATICA ACAD. SCI. U.S.A. 93:3132-3137(1996).
PROG. NATICA PROPERN.
SEQUENCE 125 AN: 13007 MM; CA70D20C CRC32;
        US-08-468-011A-2.rspt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT OF 1991 PRELIMINARY; PRT; 1904 AA. AC 08919. TO 09919. PRELIMINARY; PRT; 1904 AA. AC 08919. TO 09919. TO 0991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-HAJARY.
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STRAINH-MARY.
STRAINH-MARY.
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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|||||||||
173 HCTRNYIH 180
                                                                                                                                                                                               Tue Nov 24 08:11:01 1998
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SERRIFIE-OB 13264.

GARRIN D., BANET C., MARTINEAU B., GGZEO J., CAVIN J.F., DIVIES C., FUN GARRIN D., MARTINEAU B., GGZEO J., CAVIN J.F., DIVIES C., FUN GARRIN D., MARTINEAU B., GGZEO J., CAVIN J.F., DIVIES C., FUN GARRIN CATIVITI: 2.AMINO-1(3-0XOPROP-2-ENVL)-BUT-2-ENEDIOATE BENEL, X93091, E214715, ...

ENGLAND CONTROL OF THE CATIVITY OF THE C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13% Score 7; DB 2; Length 252; Best Local Similarity 100:09; Pred. No. 2,228-00; Best Local Similarity 100:09; O; Mismatches 0; Indels Market Dec. 7; Conservative 0; Mismatches 0; Indels Market Dec. 90; Mismatches 0; Mismatches 0
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DOGGOTO PRELIMINARY; PRT; 229 AA.

DOGGOTO PRELIMINARY; PRT; 229 AA.

DOT 01-000-1996 (TREMELEEL, 01, CREATED)

DT 01-1000-1996 (TREMELEEL, 01, LAST SEQUENCE UPDATE)

DT 01-1001-1996 (TREMELEEL, 01, LAST ANNOTATION UPDATE)

DE CREMENSORE XII COSMID 8084. ANNOTATION UPDATE)

GN SACCHAROCHES CREWISINE (BAREN'S IMBATS.)

CC EURAROCH; FUNGI, SCOMFOCTINA; HEMIASCOMFCETES.

RP SEQUENCE FROM N.A.

RC STRAINSCHEE FROM N.A.

RX HEMILES STRAINSCHEE (ABREN'S TREAT)

RX HEMILES STRAINSCHEE (ABREN'S TREATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHT C. S. CHOM H.P. OU J.T.;
SUBMITTED (MAR-1959) TO EMEL/CHRBANK/DDBJ DATA BANKS.
BEDL. AFOSG-96: G3046603;
HFOFTHETAL PROENTH. PLASTER PLASTER SEQUENCE J.S. AM. 29176 MR. 30APBPCS CRG32.
                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 LFVSFML 106
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Tue Nov 24 08:11:01 1998
                                                                                                                                                                                                                                                  19 SLTATSL 25
                                                                                                                                                                                                                                                                                                                     485 SLTATSL 491
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                                                                                                                                                                 Matches
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      Page 29
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                                                                                                                                                                                                                                                                                                                                                                                                             STRANTO-COGODISCO, STRONE H. TANKA A., ASANIZO E., NAKANDRA Y., RANKO C., CORDON C., STRONA T., SASANOTO S., KIHODA, TKINDRA B., TANKA M. M., SASANOTO S., KIHODA, TKINDRA S., TANKA M. M., MATRODA M., TANKA M., MATRODA M., TANKA M., TANK
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1.34, Score 7; DB 3; Length 229;
Merchea Similarity 100:04: Pred Me. 2.72+00;
Matchea 7; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels 0; Gaps
US-08-468-011A-2.rspt
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Best Local Similarity 100.0%; Pred. No. 2.22e+00;
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SENDICIBELLA FIRMICITES, LOW G+C GRAM-POSITIVE BACTERIA, LACTOBACILLACEAE, OENOCOCCUS.
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ND 1994897

ND 1994897

PER 1994897

PER 1994897

PER 1994897

PER 1994897

PER 1994897

PER 199987

PERSENEEL 03. LAST SEQUENCE UPARTS

DT 01-WW-19997

PERSENEEL 03. LAST SEQUENCE UPARTS

DT 01-WW-19997

PER 199987

PER 19
                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-PCC6803;
THANTS S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SECURNCE FROM N.A.
STRAINGS ME (AB972);
WATESTOR N.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQUENCE FROM N.A.
GTALANE-218C (A8972);
GTALANE-218C (A8972);
GURRAT J. M.;
GURRAT TO (SEP-209);
DEMIL, 1197129; G425099;
SEQUENCE 229 As; 25696 PW; 4E7F3346 CRC12;
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SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
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STRAIN-S288C (AB972);
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||||||||
287 PAAFVAA 293
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SERALP-6693-1.
NOORD P. P.A. TANG L., YOON Y.J., NING S., MUELLER R., HUTCHINSON C.R.,
TLOSS H.G.,
SUBMITTED (120-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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1.3%; Score 7; DB 5; Length 400;
Bert Local Similarity 100:04; Pred. No. 2.728-40;
Marches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
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EUTRYNOTA: JAHLALIA; PROTOZOA: SARCOMASTIGOPHORA: MASTIGOPHORA;
COMARTIGOPHORA: KINETOPLASTIDA: TRYPANGODMATIDAE.
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D 022372
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D 01-10911999 (TREDELIEL. 06, LAFT SEQUENCE UPDATE)
D 01-10711999 (TREDELIEL. 06, LAFT SEQUENCE UPDATE)
D 01-10711999 (TREDELIEL. 06, LAFT SEQUENCE UPDATE)
D 01-10711999 (TREDELIEL. 06, LAFT SEQUENCE UPDATE)
D 01-1071199 (TREDELIEL. 06, LAFT SEQUENCE DE DATE OF SEQUENCE PERM N.A.
D 02-1071199 (TREDELIEL. 06, LAFT SEQUENCE PERM N.A.
D 03-1071199 (TREDELIEL. 06, LAFT SEQUENCE PERM N.A.
D 03-1071199 (TREDELIEL. 06, LANDA S., FLOSS H.G.;
D 03-1071199 (TREDELIEL. 06, LANDA S., MUTCHINSON C. R., TATLOR M., MOFFRANN D., TOON Y.J., NING S., MUTCHINSON C. R., TATLOR M., MOFFRANN D., TOON Y.J., NING S., MUTCHINSON C. R., TREST SEQUENCE PROM N.A.
THE SEQUENCE 
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 Query Match
1.34; Score 7; DB 3; Length 420;
Best Local Similarity 100.04; Pred. No. 2.724-00.
Natches 7; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.3%; Score 7; DB 5; Length 291; Bet Longth 200.0, Pred. No. 2.725-40; Hatches 7; Conservative 0; Mismatches 0 Indels Matches 7; Conservative 0. Mismatches 0.
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DO 59583.

DO 59583.

DO 59583.

DO 59583.

DO 70 01-MC-2959 (TREMBLEEL 07, CRAATE)

DT 01-MC-2959 (TREMBLEEL 07, LAST SEQUENCE UPDATE)

DT 21-MC-2959 (TREMBLEEL 07, LAST SEQUENCE UPDATE)

DT 210-MC-2959 (TREMBLEEL 07, LAST SEQUENCE UPDATE)

SEGUENCE FROM N. A.

RC STRAIN-MCC-4958, N. A.

RC STRAIN-MCC-4958, N. A.

RC STRAIN-MCC-4958, TO EMBL/GERRANK/DDBJ DATA BANKS.

RE SEGUENCE FROM N. A.

RC STRAIN-MCC-4958, TO EMBL/GERRANK/DDBJ DATA BANKS.

RE SEGUENCE FROM N. A.

SEGUENCE FROM N. 
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WATERSON R., S.
SUBHITTED (JUL.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
BRD. AFOLGATO. 229211/6; A
SEQUENCE 731 AA. 34059 MM; 5413E006 CRC32;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINERSTOOL AND SECR C.;
SUBLICH J. WORLDWARN P., BECR C.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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OC ETGNATIOSPHORA, KINETOPLASTIDA, TRYPANGSMATINA, FR

RU [1]

RE SEQUENCE FROM 1A.

RX MDLINE: 9100722.

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| | | | | | | |
OY 153 SISFGSL 159
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464 QVAAAHA 470
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ID Q22659
AC Q22659;
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Page 33
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ID 026644
DO 026444
DO 026
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Best Local Similarity 100.04, Pred. No. 7.23e-00;
Best Comervative 0; Minmatches 0; Indels 0; Caps 0;
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133, Score 7, DB 2, Length 351;
Best Local Similarity 100:09, Pred 100 - 7.12e-00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                                                                                                                                                                                                 054458
PRELIMINARY: PRT; 290 AA.
054458
01-JUN-1999 (TREMBLER: 06. CREATOR
01-JUN-1999 (TREMBLER: 06. LAST SEQUENCE UPDATE)
01-JUN-1999 (TREMBLER: 07. LAST ANNOTATION UPDATE)
HYDOMERICAL 32.1 KDA PROTEIN.
FROMEN REBRICOLA.
FRANKINGER: SACCIOSACTERIA: PACULATIVELE ANARROBIC RODS;
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EUKARYOTA: METAZOA; ACOELONATES; NEMATODA; SECERNENTEA; RHABDITIDA.
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1.3; Score 7; DB 5; Length 398;
Best Local Similarity 100.04; Pred. No. 7.22=+00;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE SOURCE C. XIA T. JENSEN R.A.;
GUBRANANIAN P.S. XIE G. XIA T. JENSEN R.A.;
FACTERIOL 180.115-127(1598).
SEQUENCE 290 AA: 32110 MM; BBAAS484 CRC212,
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MONOOXYGENASE.
SEQUENCE 351 AA; 30512 MM; A0D6B09D CRC32;
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| 489 TSLYLAM 495
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296 VARATEA 302
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                    153 SISFGSL 159
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The Nov 24 08:11:01 1998 US-08-468-011A-2.rapt	DT 01-NG-1998 (TREMBLAZL. 07, LAST ANNOTATION UPDATE)  201 STATES AND STATEM.  202 CENTRANCOLA. METAZOA, ACOELOMATES, NEWATODA, SECENERITEA, RHABDITIDA.  203 CHARNOTAL METAZOA, ACOELOMATES, NEWATODA, SECENERITEA, RHABDITIDA.  204 CHARNOTAL STANSCOORER. A.  205 CHARNOTAL ANNOCACIONER. AND STATEM. A.  206 CHARNOTAL ANNOCACIONER. AND STATEM. A.  206 CHARNOTAL ANNOCACIONER. AND STATEM. A.  207 CHARNOTAL ANNOCACIONER. AND STATEM. A.  208 CHARNOTAL ANNOCACIONER. A.  208 CHARNOTAL ANNOCACIONER. A.  208 CHARNOTAL ANNOCACIONER. A.  208 CHARNOTAL A.  208 CHARNOTAL ANNOCACIONER. A.  208 CHARNOTAL A.  209 CHARNOTAL A.  209 CHARNOTAL A.  209 CHARNOTAL A.  209 CHARNOTAL A.  200 CHARN	THE NOW 24 08:11:01 1998 (TREMBLEEL. 07, CREATED)  DI -AUG-1998 (TREMBLEEL. 07, CREATED)  DI -AUG-1998 (TREMBLEEL. 07, LAST SEQUENCE UPDATE)  OL-AUG-1998 (TREMBLEEL. 07, LAST SEQUENCE UPDATE)  NA SEQUENCE FROM N.A.  NA SEQUENCE SEGUENCE
Page 37 Tue Nov 24 0	DO 01-NO DD RESSOR DD RESSOR R	Page 39  Tue Nov 24 08  DT 01-NU DT 01-
The Nov 24 08:11:01 1998 US-08-468-011A-2.rzpt	DI 01-NOV-1996 (TREBELEEL. 01, CREATED) DI 01-NOV-1996 (TREBELEEL. 01, LAST SEQUENCE UPDATE) DI 01-NOV-1996 (TREBELEEL. 06, LAST ANNOTATION UPDATE) DI 01-NOV-1996 (TREBELEEL. 06, LAST ANNOTATION UPDATE) REAL TOTAL TO	DESCRIPTIONACEAE.  10 C. VIBRIONACEAE.  10 C. VIBRIONACEAE.  11 C. VIBRIONACEAE.  12 DESCRIPTIONACEAE.  13 DESCRIPTIONACEAE.  14 DESCRIPTIONACEAE.  14 DESCRIPTIONACEAE.  15 DESCRIPTIONACEAE.  15 DESCRIPTIONACEAE.  16 DESCRIPTIONACEAE.  17 CONSERVATION ON: PECA No. 220-05 angeh 448; Marches O; Indels O; Gaps O; Marches O; Indels O; Caps O; Marches O; Indels O; Caps O; Marches O; Marches O; Marches O; Indels O; Caps O; Marches O; D; Marches O; D;

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HIGGORY B. ANDERGON K., BAVHES C., BERKS M., BONFIELD J.,
BIRTON J. (CONTENT, M., CONCERT, J., COLLIGON, A., ENCYTON, R.,
DEAR S., DUT S., DUTSTIN R., PAYELLO A., FULLON I., CARBORRA RAKES P.,
HAMKINS T., HILLIER L., JIER M., JOHNSTON I., JONES M., KERSIAN, J.,
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KARYOTA, PAMYRI, BRORKOPHYTA, ANGIOSPERMAE; DICOTYLEDONEAE;
PAMALES, CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.3%; Score 7; DB 10; Length 806;
Best Local Similarity 100.0%; Pred. No. 2.22e-00;
Matches 7; Conservative 0; Mismatches 0; Indela
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                                                                                                                                                                                                                                                                                                               Query Match 1.3; Score 7; DB 2; Length 564, Bect Local Similarity 100.04, Pred No. 2.22++00; Matches 7; Conservative 0; Hismatches 0. Indel
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SEQUENCE PROM N.A.
RATRAINSCY. COLUMBIA:
SUBMITTED (APR-1998) TO EMBL/CENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CADURENCE FROM N.A.
STRAIM—CV. COLUMBIA;
SURMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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STRAITS. COLOMBIA:
WATESTOR R.;
SUBMITIED (APR.199) TO EMEL/GENBANK/DDBJ DAIR BANKS.
EMEL: APOSESS; G3047068 - 44132ECC CRC32;
SEQUENCE 806 AA; 91191 MM; 44132ECC CRC32;
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SWIE R.,
SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DAIN BANKS.
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4 LGASLHV 10
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F7N22.10.
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                   Tue Nov 24 08:11:01 1998
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                   Page 41
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RA REEGON W. CORACKBREEGON D. DOESON R. KHALK M. G. CLODERSON S.,
RA CHOTUS A. RECHREGEON D. DOESON R. KHALK M. G. CLODERSON S.,
RA KKERNEY K. F. FITGERALD L. M. LEE N. ADAKS M. D. HICKTE E. K.
RA REED D.E. GCAPHEN D.D. WITTERBACK T. R. PETERSON D. RELLEY J.M.,
RA COTTON M.D. WILDRAW J. M., FUJII C., DOMBAN C., MATTER L., MALLIN B.,
RA VERES W.S., DOSDONOWER M., KANP P.D., SMITH H.O., FRASER C.M.,
R. WINTEN B.S. S. C. (1967) (1997).
R. PERL, MOOROSIS (231) (1995).
R. PERL, MOOROSIS (231) (1995).
SERL, MOOROSIS (231) (1995).
SERL, MOOROSIS (231) (1995).
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SERVINCE COROLL S. MAKAWIR E., MAKHIU E., MAKAWIR T., STOP, S. (COTMI E., TANKKA A., ASAMIRU E., MAKAWIRA T.,
HITALINA N., HIROSANA N., SUGIURA M., SIAGNOTO S., FILHURA T.,
MATSHAN S., TAKEGUHI C., WADA T., WATANABE N., TAMODA M., YASUDA M.,
TERMY S.;
S. (109-118(1996).
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GALIGOS CALLIOS (CHICKEN).
EUKANOCA: BETRAODA; AVES; NEGGNATHAE;
GALLIPORNES.
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RE STORINGE FROM N.A.

STAINMAILTE LEGRERSH TISSUE-BRAIN;

RA FALLES J. ROSEN K.M. CORFAG C. LANE W.S., FISCHBACH G.D.;

R. THENGELING, STAINMAILES AND ACTUAL STAINMAILE SEGUELING PORTH.

PREME, PROGOTIE: PROGOTIS ECF 1.

PRAY, PROGOTIS ECF 1.

PROGOTIS ECF 1.

PROGOTIS ECF 1.

PROGOTIS ECF 1.

PROFOTIS ECF 
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                                                                                                                                                                                                Query Match 13%; Score 7; DB 13; Length 602; Best Local Similarity 100:0; Pred. No. 2.22e-00; Destroches 0; Conservative 0; Mismatches 0; Indels
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TO 12-121

TO 12-121-131

TO 12-121-1397 (TEREBLEEL O.) CREATED)

TO 14-121-1397 (TEREBLEEL O.) CREATED)

TO 14-121-1397 (TEREBLEEL O.) LAST SKOUTCE UPDATE)

TO 14-121-1397 (TEREBLEEL O.) LAST SKOUTCE UPDATE)

TO 14-121-1399 (TEREBLEEL O.) LAST SKOUTCE UPDATE)

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TO 14-1399 (TEREBLEEL O.) LAST SKOUTCE O. LAST SKOUTCE ENDATE)

TO 15-1399 (TEREBLEEL O.) LAST SKOUTCE O. LAST SKOUTCE ENDATE)

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TO 15-1399 (1966)

TO 15-1399 (1966)

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STRAIN-ECCEGO3;
TARATA S.:
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 302 ISFGSLA 308
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Tue Nov 24 08:11:01 1998
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Page 46
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Best Local Similarity 10:0%; Pred. No. 2.22d-00; Indels 0; Gaps
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                            US-08-468-011A-2.rspt
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                                                                                                                Query Match 1.3%; Score 7; DB 10; Length 1126; Best Local Similarity 100,0%; Pred. No. 2.228+00; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.1%; Score 6; DB 5; Length 37; Best Local Similarity 100:09; Pred. 100. 1.574-02; Matches 5; Conservative 0; Mismatches 0; Indels Matches 10; Conservative 0; Mismatches 0; Indels
                                               RA THEOLOGIS;
RE SUBMILLS OUN-1999) TO EMBL/CENBANK/DDBJ DATA BANKS
REMEL, ACOOSS'11; 63176590; -.
SQ SEQUENCE 1126 AA; 126148 MM; 9378°C620 CRC32;
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                                                                                                                                                                 499 TVRVLAT 505
                                                                                                                                                                                        Qy 336 TVRVLAT 342
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  Tue Nov 24 08:11:01 1998
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| | | | | | |
Qy 203 AHIGVK 208
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Page 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SÉCURNE FROM N. N. SCHKARTE J.R., TORIDMI M., YU G., KWAN A., OJI O., VYGOSSKALN-Y. S., SCHKARTE J.R., TORIDMI M., YU G., KWAN A., OJI O., LIU S., LI J., ARAJOO R., W. M., BERNEDER Y., CONNAY A.B., CONNAY A.B., CONNAY A.B., DAWAR K., PENG J., KIN C., KURTE D., LI Y., PALM. T., PALM. S. W., ECKER J. R., PENGESPEE N. A., THEOLOGIS A., SHINN P., SUN R., DAVIS R. W., ECKER J. R., PENGESPEE N. A., THEOLOGIS A., SHINN P., SUN C. (DEC.1997), TO ENGL/GENBARK/DBSJ DAYAR BARKS.
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1.3%; Score 7; DB 5; Length 873;
Bert Local Stanlarity 10.0%; Pred. No. 2.22e-0.0
Bert Local Stanlarity 0; Mismatches 0; Indels 0; Gaps
Macrhes 7; Conservative 0; Mismatches 0; Indels 0; Gaps
                                          US-08-468-011A-2.rspt
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                                                                                                                                                                                                                                                                                                                                                                                                    ATRIDOPEIS THALIANA (MOUSE-EAR CRESS).
EURARFONES, PLANTA, FIGHROPHYTA: ANGIOSPERNAE; DICOTYLEDONEAE;
CAPPARLES, CRUCIFERRAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.1%; Score 6; DB 14; Length 27;
Best Local Similarity 100,0%; Pred. No. 1.574-02;
Matches 6; Conservative 0; Mismatches 0; Indels
Matches 6; Conservative 0; Mismatches 0; Indels
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AD 066270.

DT 0674270.

DT 01-000-1396 (TREMELREL. 01. CREATED)

DT 01-000-1396 (TREMELREL. 01. LAST SEQUENCE UPDATE)

DT 01-000-1396 (TREMELREL. 01. LAST SEQUENCE UPDATE)

DT 01-000-1396 (TREMELREL. 01. LAST SEQUENCE UPDATE)

DT 01-000-1396 (TREMELREL. 01. LAST ANNOTATION UPDATE)

DT 01-000-1396 (TREMELREL. 01. LAST ANNOTATION UPDATE)

CUCUMBER MOSAIC VIRUS (GRV).

CUCUMBER MOSAIC VIRUS (GRV).

CUCUMBER MOSAIC SEGUENCE FROM N.A.

RESUCUENCE FROM N.A.

RESUCUENCE FROM N.A.

RESUCUENCE 164.136-1391; 1989).

RESUCUENCE 164.136-1391; 1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LATECTORY OF THE STOR N.A.
STRAINCE FROM N.A.
STRAINCHOGUS A.;
STENITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THEOLOGIS A.; SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                ULT 36
004605
004605
004605
00406-1999 (TREMELREL, 07. CREATED)
00-MOG-1999 (TREMELREL, 07. LAST SEQUENCE UPDATE)
P1001-SUG-1999 (TREMELREL, 07. LAST ANNOTATION UPDATE)
P1001.15 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 I. I. I. SEQUENCE FROM N.A.
C. STRAINES.
C. STRAINES.
D. HINDA S., HANDA K., ISHIRAMA K., HIURA K.;
L. VIROLOGY 164:336-331(1989).
R. RELL MORGHE, GR080723;
C. SEQUENCE 27 AA; 2783 MM; DA37EACE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                              Tue Nov 24 08:11:01 1998
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||||||
Qy 256 VEGLYL 261
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LITTORING FROM N.A. STRAINACC 35210 / B31, WEDLINE, 90665943. FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,

Query Match 1.1%; Score 6; DB 2; Length 33; Best Local Similarity 100.0%; Pred. No. 1.57e+02;

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Page 52
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STRAIN-PRISON, M.S.
STRAIN-PRISON, M.S.
HEDLINE, 94150716
H. MILGOR R., ANDERSON K., BAYNES C., BERKS M., COULGON A., BONTELD J., BURNOON J., CONFELL M., COPPET T., COOPER J., COLLEGN A., CRAXTON M., DERK M., OBLAS C., DUBLING M., PLINLING M., CANDERS A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., CANDERS A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.1%: Score 6; DB 6; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.570-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-468-011A-2.rspt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.1%; Score 6; DB 10; Length 57; Bet Local Similarity 100; 0%; Pred No. 1.57e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-468-011A-2.rspt
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1.1%; Score 6; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.57e+02;
Destructuse 6; Conservative 0; Mismatches 0; Indel
                                                                                                                                                               ESSULT. 44
10.44667 PRELIMINARY: PRT: 59 AA.
10.4007-1396 (TREBILER. 01. CREATE)
10.4007-1396 (TREBILER. 01. CREATE)
10.4007-1396 (TREBILER. 07. LAST ESDUREN UPDAIR)
10.4007-1396 (TREBILER. 07. LAST ESDUREN UPDAIR)
10.4007-1398 (TREBILER. 07. LAST ENGURATION UPDAIR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tue Nov 24 08:11:01 1998
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208 KELESL 213
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| | | | | | |
Qy 352 HDTRKQ 357
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      Page 49
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PROKANTORA: GRACILICUTES: SCOTOBACTERIA; FACULANTIVELY ANAEROBIC RODS;
VIBONACEAE.
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10 04445;

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TISSUEDHEN SERDS OF A THALIANA ECOTYPE COLDMBIA;
NANNAL M., GRELLET F., LANDIE M., NETER Y., COCKE R., DELSENT M.;
SUBMITTED (CCT-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUEDNE SERSO PO THALLANA ECCIPPE COLUMBIA;
MARNAL M., GERLLET F., LANDIE M., NETER Y., COOKE R., DELSENT M.;
SUBMITTED (FEB-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
US-08-468-011A-2.rspt
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1.13; Score 6; DB 2; Length 59;
Bacches Score 10: On Hamatches 0; Indexe
b 13 Leverh 18
y 193 Leverh 18
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STRAIN-MANO;
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330 FILFLN 335
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Page 53

US-08-468-011A-2.rspt

Tue Nov 24 08:11:01 1998

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REBULT 49

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D 07
                                                                AN THERRY-HIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
R. MATEGON M., PETISCHOOK L., WILKINSON-SPROAT J., WOHLDMAN P.;
R. MATEGON M., PETISCHOOK L., WILKINSON-SPROAT J., WOHLDMAN P.;
R. MATEGON M., PETISCHOOK L., WILKINSON-SPROAT J., WOHLDMAN P.;
R. STATINSELSTON M.;
R. STATINSER M.;
R. STATINSELSTON M.;
R. STA
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Qy 288 AAFVAA 293
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DE 061383
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DE 07.AGC-1999 (TREMBLEEL 07, LAST SEQUENCE UPDATE)
DE 07.20C-1999 (TREMBLEEL 07, LAST SEQUENCE UPDATE)
DE 07.20C-1999 (TREMBLEEL 07, LAST SEQUENCE UPDATE)
DE 07.20C-1999 (TREMBLEEL 07, LAST ANNOTATION UPDATE)
DE 07.20C-1999 (TREMBLEEL 07, LAST ANNOTATION UPDATE)
DE 07.20C-1999 (TREMBLEEL 07, LAST ANNOTATION UPDATE)
DE 07.20C-1999 (TREMBLEEL 07, LAST AND UPDATE)
DE 07.20C-1990 (TREMBLEER 07, STADER 
JONES M. KERSHAN J., KIRSTEN J. LAISTER N. LATREILLE P.
LICHTRING J. LLOYD C. WERHERAY M. MOSTHOMER B. O'CLIAGGAN M.
PARSONS J., PERCY C., RIFREN L., ROCPEA A., SAUNDERS D., SHOWHERE N.,
ENALDON N., SHITH A., SOUNDAMBER E. STADER N. SILSTON J.
HILERY-HIGG J., THOMAS K., VANDIN M., VANCHAN K., WATERSTON R.,
MATERS A., SHISSTOCK L., MIKINSON-SPROAT J., WOHLDMAN P.;
RATHER SEG J. THOMAS K., VANDIN M., VANCHAN R.,
SEGDENE FROM N.A.
SCHALLP-BALSCOL N.)
GORLA D., SCHEET P.,
SCHALLP-BALSCOL N.)
[3] SHITTED (MAY-1998) TO EMEL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAINTH-BRISOLU NI;
HEDLINES 94150718
HELLONE E. MISSCOORE R., ANDERSON K., BANTES C., BERKS M., COULSON A., SCHANTON M., BENKSON G., DONERLH M., COPERT T., COOPER J., COULSON A., CENATON M., DEAR N., ON C., DURBRIN R., PATSCOOR M., ALONE N., CRESH W., MISSTRIN M., ALSTER M., DANTON M., DONEROW L., LLOTTON C., HEDRINAY A., MOSTIDONE B., O'CALLAGIAN M., PARSONS J., PREFOR C., MITTER M., DONER M., SCHOWERE B., O'CALLAGIAN M., SMALDON N., SMITH A., SONNHAMERR E., STADER N., SURFERON J., RONNHAMER R., STATER M., SHOWNEES D., O'CALLAGIAN M., SMALDON N., SMITH A., SONNHAMER R., STATER M., SHOWNEES D., SHOWNEES D., SHOWNEES D., SHOWNEES D., SHOWNEES D., SHOWNEES R., STATER M., SONNHAMER R., STATER M., SHOWNEES D., SHOWNEES R., STATER M., SHOWNEES D., SHOWNEES D., SHOWNEES R., STATER M., SONNHAMER R., STATER M., SHOWNEES D., SHOWNEES R., STATER M., SHOWNEES D., SHOWNEES R., STATER M., SHOWNEES R., STATER M., SHOWNEES R., STATER M., SHOWNEES D., SHOWNEES R., STATER M., SHOWNEES R., STATER M., SHOWNEES R., STATER M., SHOWNEES D., SHOWNEES R., STATER M., SHOWNEES R., SHOWNEES R., STATER M., SHOWNEES R., SHOWNEES R., SHOWNEES R., SHOWNEES
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ö 0; Mismatches 0; Indels 0; Gaps Matches 6; Conservative

Oy 222 SIEATS 227 41 SIEATS 46

ö Query Match 11M: Score 6; DB 2; Length 75; Best Locks Similarity 100:04; Pred. No. 1.57+02; Indels Marches 6; Conservative 0; Minasches 0; Indels

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43 STLVLV 48 | | | | | | | 364 STLVLV 369 a

Search completed: Mon Nov 23 13:45:10 1998 Job time : 153 secs.

Page 55

Query Match 1.1%; Score 6; DB 10; Length 75; Best Local Similarity 100.0%; Pred. No. 1.57e+02;

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Database:

Post-processing:

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67.0 KD PROTEIN IN PRO	DEVELOPMENTAL PROTEIN	WINA REDEAT DECTRING	SERUM ALBUMIN PRECURSO	NADH-UBIQUINONE OXIDOR	SERUM ALBUMIN PRECURSO	SERUM ALBUMIN PRECURSO	REPLICATION PROTEIN EL	HIPOTHETICAL 67.7 KD P	SET-DETACE ONCOCEUS S	HYDOTHETICAL 72 9 KD D	CYSTEINYL-TRNA SYNTHET	SAC2 PROTEIN.	PUTATIVE CEL OPERON RE	HEAT SHOCK COGNATE 70	PUTATIVE CYSTATHIONINE	HIPOTHETICAL 69.8 KD P	MADE TRACEPTOR PAR	KINESIN-LIKE PROTEIN N	HYPOTHETICAL 76.9 KD P	HOMEOTIC PROTEIN ORTHO	HYPOTHETICAL 69.7 KD P	HIPOTHETICAL S/ 3 KD P	SKI-RELATED ONCOGENE S	GLYCYL-TRNA SYNTHETASE	HYPOTHETICAL 75.5 KD P	HYPOTHETICAL 74.2 KD P	CELL DIVISION PROTEIN	LACTOTRANSFERRIN PRECU	HYPOTHETICAL 79.5 KD P	PHOSPHATE ACETYLTRANSF		MEGENTURICAL WING TOWN		EXOPOLIGALACTURONATE L		CAPSID PROTEIN	CAPSID PROTEIN	OUTER CAPSID PROTEIN V	MANAGE	SPHOFRUCTOKINASE	REATH-CADRERIN DRECTES
THJW_ECOLI	GV7_XENLA	WD42 DICDI	ALB MACATE	NUSH BALMU	ALBU_RAT	z			TEND LEAST				CELR_BACSU	HS72_LYCES	METX YEAST	TITE MICIO	MISW COOL	NOD DROME	YMIB_YEAST	HMOC_DRONE	YODY MYCTU	PDOC WARD	SNON HUMAN	SYGB_ECOLI	YKO6_YEAST	TX05 MYCTU	FTSH MYCGE	TRFL_BOVIN	YRFF_ECOLI	PTA_ECOLI	PBPF_BACSU	MEST LETTINE	FOG DROME	PELX_ERWCH	YKH2_YEAST	VP4_NCDV	WP4_ROIBC	VP4 POTSE	TAND POOL	K6PP RABIT	CADC HUMAN
144																																									
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THE ROY 24 08:111:00 1998  CC -1- FUNCTION: THIS 16 A SPECIFIC RECEPCOR FOR PARATHEROID HORMORE. THE ACTIVITY OF THIS RECEPOR 15 MEDIATED BY OFFICEN WHICH ACTIVATE CC. T. STISSUE SPECIFICATION: COPIED RECEPORS.  CC -1- SINITALIZITY: EXCHANGES TO PAMILY 2 OF G-PROTEIN COPIED RECEPORS.  DR MIN: 00146; -19 CAPACITY SETSUE 27-2; 1.  DR MIN: 00146; -19 CAPACITY SETSUE 27-2; 1.  FINE FROM THE FROM THE FROM THE FORM THE FORM THE FROM THE	The Nov 24 06/11:00 1998  The Nov 24 06/11:00 1998  THE DOMAIN 299 273 CTTOPLASHIC (POTENTIAL).  FOR TANSERS 24 24 24 24 24 24 24 24 24 24 24 24 24
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A EXPLISE (503)219 P. ERANG X.Y., FROLIK C.A., HARVET A.,

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SEQUENCE PRINCES.
MEDINE: 9535443.
BIOCHEL BIOPHYS. RES. COMMUN. 212:204-211(1995).
                                                                                                                                                                                    MEDLINE; 95169147.
JIANG S., ULAICH C.D.;
BIOCHEM. BIOPHYS. RES. COMMUN. 207:883-890(1995)
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TISSUE-LUNG;
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SEQUENCE FROM N.A.

MEDLINE: 31766990.

ISHIRBAT., MARANARA S., KAZIRO Y., TAKAHASHI T., TAKAHASHI K.,

MAGATAR J., MASHARA T., MASHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT TO STANDARD: PRI; 440 AA.

D STANDARD: CARSOLISED TO STANDARD: PRI; 440 AA.

D STANDARD: CARSOLISED TO STANDARD: CARSOL
                                                                                                                                             PIR; AJ9286; AJ9286.

GCRD; GCR, DOJG.

PROSITE; PEOGESO: G. PROTEIN_PREEP_F2_1; 1.

PROSITE; PEOGESO: G. PROTEIN_PREEP_F2_2; 1.

G-PROTEIN COUPLED RECEFORS; TANKSHERGRANE; GLYCOPROTEIN; SIGNAL.

26 POTENTAL.
       US-08-468-011A-2.rsp
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01.NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01.NOV-1991 (REL. 22, LAST ANNONATION UPDATE)
SECRETIN RECEPTOR PRECURSOR (SCT.*R).
RATTER NONVEXCIUG (RAT).
EUTHERNA'S RODENTIA.
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EXTRACELLULAR (POTENTIAL).
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158 188 POTENTIAL.
159 183 POTENTIAL.
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CONFLICT 333 333 E -> G (IN REF 3).
CONFLICT 377 377 G -> A (IN REF 1).
SEQUENCE 440 AA; 50206 MH; B8CF53E4 CRC32.
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SÉGUENCE FROM N.A. TISSECATUBET: HEDLINE: 3213641. SCHIPMI E., KARGA H., KARAPLIS A.C., POTTS J.T. JR., KROMENBERG H.M., ABOUC-SHARA A. B.B., SEGRE G.V., UUEPPHER H.; 17) | RESULT | 9 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 Query Match 334, Score 18; DB 1; Length 591; Best Local Similarity 100:09; Pred. No. 1.11te-01; Lindea Metches 0; Mismatches 0; Lindea Metches 0; Mismatches TRANSMEM
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PROLINE 14 BOUNDON J., CLAYTON D., MATTEI M.G., SELDIN M.F.,
ANGICE N. RYMERE M. SEPRER J., LEVAR G., SEPRER C.;
TOWNSTON THIS IS A RECEPTOR FOR PARATHROID HORMONE AND FOR
THE PROFESSION THIS IS A RECEPTOR FOR PARATHROID HORMONE AND FOR
TREATMENT DE HORMONE PROPERS. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY OPPOSEING WHICH ACTIVITY AND MATHER
CITCLARE AND ALSO A PROSPENTATIONING—CALCIUM SECOND MESSERGER

TABOURNOSTINES DE STATUS DE L'ANTIGONE ET, FREEMAN H.W., KONG X.-P., AND SAND SANDAN A.B., UUZEPPRER H., FORCE T., FREEMAN H.W., KONG X.-P., RONNERANTE D.W., POTTS J.T. JR. KONSTROREN H.W., SEDER G.W., 1907 S.J. J. JR. KONSTROREN H.W., SEDER G.W., 1917 S.J. JR. S.J. G.C., NATL. ACAD. SCT. U.S.A. 89:2713-2715(1992).

RATIUS NORVEZICUS (RAT). EUKANYOTA, HETIZOA, CHORDATA; VERTEBRATA; TETRAPODA; HAMMALIA; EUTHREIA, RODENTIA.

SEQUENCE PROM N.A. TISSUE-BONE;

SYSTEM.

1. SUDCELLULAR LOCATION: INTEGRAL MEMBANE PROTEIN.

1. SINILARITY: BELGAGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

EMB. 13734, G46315; 
EMB. 177184, G706035; 
PROSITE: PSO6049; 
EMB. CRASS C

Page 32

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Page 36
       Page 34
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PROSTER: PROOFS!0. G-PROTEIN RECEP P2 1. 1.

G-PROTEIN COUPLED RECEPTOR; TRANSHERBARE; GLYCOPROTEIN.
       US-08-468-011A-2.rsp
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DE 0471294 STANDARD: PRT: 455 AA.

DE 0471294 STANDARD: PRT: 455 AA.

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DE 0471295 STEEL 13. CREATED)

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DE 047129 STANDARD: LAST SEQUENCE UPPARTS

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Pred. No. 3.17e+25;
0; Mismatches 0; Indels
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| 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 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SCHNEIDER H., FEYEN J.-H., RAO MOVVA N.;
EUR. J. PHARMACOL. 246:149-155(1993).
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TISSUE-KIDNEY;
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01-APR-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 35, LAST ANNORATION UPDATE)
VASACATUR INTESTINAL POLYPETINE RECEPPOR 1 PRECHESOR (VIP-R-1)
VILLIARY ADDRIVINE CYCLASE ACTURA RECEPPOR 1 PRECHESOR (VIP-R-1)
(PRAAP TYPE II RECEPPOR) (PACAP-R-2).
                                                                                                                                            PROSITE; PSO0649; G.PROTEIN RECEP_P2_1; 1.
PROSITE; PSO0640; G.PROTEIN RECEP_P2_2; 1.
ALTERNET PROSIDED RECEPTOR: TRANSHEMBRANE; GLYCOPROTEIN; SIGNAL;
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ISBILINE, TOTALISE TO WORL K., TAKHASHI K., NACATA S.,
RETRON 8:811-815(1393).
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2.4; Score 13; DB 1; Length 457;
Best Local Shilarity 100,04; Pred. No. 5.28e-16; Indels
Matches 13; Conservative 0; Mismatches 0; Indels
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Page 37
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ZHANG, K.R. SMITH D.P., HYSIOP P.A., HEIDAN M.L., HASSAN H.A.,
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"STANDAR J. SHOOKES, OF PROTEIN RECEPTOR.

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RE TISSUE-LIVER A. ATTAR N., ELSHOURBACK N.A.; DATA BANKS.

AGANON A. M., ATTAR N., ELSHOURBACK N.A.; DATA BANKS.

RESPONDED TO THE SERVICE OF THE SERVICE OF THE SECRETOR FOR VIP THE ACTIVITY OF THIS CONTINUE WHICH ACTIVITY ADMILLIA.

TO THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SECRETOR FOR VIP THE ACTIVITY ADMILLIA.

THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SECRETOR OF THE SERVICE OF THE 
                                                                                                                                                          (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
(PACAP TYPE II RECEPTOR) (PACAP-R-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDLINE, 94215025.
OTRIVIALA, ROUTER-FESSARD C., DARMOIL D., MAORET J.J., CARRERO I.,
OTRIVIALE E., LABUTHE M.;
OCCHEM. BIOPHYS. RES. COMMUN. 200:769-776(1994).
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Pred. No. 5.28e-16;
0: Mismatches 0; Indels 0; Gaps
US-08-468-011A-2.rsp
                                                                                                                                                                                                                                                                                         ONO SAPIENS (HUMAN).
Uranyota, hetalsoa, chordata; vertebrata; tetrapoda; mammalia;
Tyterata, primates
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EUTHERIA: ARTIODACTYLA.
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TISSOURCE FRON N.A.
TISSOURCE PRON N.A.
SEEDHARAN S. P., PATEL D.R., HUANG J.-X., GOETEL E.J.;
SECHEM: BIOPHIG: RES. COMMUN: 193:546-553 (1993).
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RACELLULAR (POTENTIAL).
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7E025D4F CRC32;
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459 AA.

PRT;

STANDARD;

RESULT 14 ID VIPR\_RAT

Query Match Best Local Similarity 100.0%; Matches 13; Conservative

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TISSUEPARCERS.
REDLINE, 9607224.
GREALINE, 9607224.
THORRUS B., VIONNET N., FROGUEL P.,
DIABRESS 84, 1202-1208(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0%; Pred. No. 4.31e-13;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saps
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GIR, UTDAN STANDARD; PRT; 466 AA.
GIR, GISHOO, C14401,
C1-FER-156 (REL. 31), CREATED)
O1-FER-1596 (REL. 31), LAST SEQUENCE UPDATE;
O1-WO-1997 (REL. 32), LAST ANDATION UPDATE;
O1-WO-1997 (REL. 32), LAST ANDATION PROCESSED
DEFINITION TO ALIPPETIDE RECURSOR (GIP-R) (GLUCOSE-
DEFINITION FOULT PETITUE RECURSOR (GIP-R) (GLUCOSE-
DEFINITION FOULT PETITUE RECURSOR (GIP-R) (GLUCOSE-
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LAKELINE, 94129399,
STRECHER C.A. NATHERES S., GRANT P.J., BIGGS S.H., WHITHORE T.E.,
GENECHER A.A., NATHERES S., GRANT P.J., BIGGS S.H., ROSENBERG G.B.,
GENECHER 140:209:1994,99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÉÉOTENCE FROM N.A.
MEDLINE; SOGUISTE, SOUSSETE, B., PERHANN H.C., BODE H.P.,
OOZE A., GORE R., LANKAZ-BUTICEREIT B., PERHANN H.C., BODE H.P.,
PERS LETT. 373:23-29(1995).
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TISSOCIATES, TRAILES, TRAILES, STRADER C.D., GRAZIANO M.P.;
MACHINE, 94121651, GORGONA, 196:328-334(1994).
                                                                                                                                                                                                                                                                                                                                                                                        Score 13; DB 1; Length 462;
Pred. No. 5.28e-16;
0; Mismatches 0; Indels 0;
    US-08-468-011A-2.rsp
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SUTANTOTA: ATAZADA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
EUTHRIOTA: PRIMATES:
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EUKARYOTA, HATALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA, PRIMATES.
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                                                                                           | 139 | 316 | 5 (POTENTIAL). | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 |
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USDIN T.B., GRUBER C., MODI W., BONNER T.I.;
SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
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Best Local Similarity 100.0%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 PRRINCIRNY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 PRRINCTRNYIHM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 PRRINCTRNYIH 173
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169 FRRINCTRNYIH 180
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TAMADA Y., HATAHI T., NAKAMURA K., KAISAKI P.J., SOMETA Y.,

RA WANG C.2., SERING S., SERING Y.,

GENOMICS 397179 (1951)

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DE BELL 199313 (116316) ...

DE BELL 199313 (116316) ...

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DE PROSITE PROCESO G. DROTEIN RECEP\_2.2; 1.

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EXTRACLILIAR (POTENTIAL). 399 V \*- NGRIDPAAAPLARRRGTAPPLGALVGQV (IN LONG FORM) C (IN REP. 2).

10 R \*- S C (IN REP. 2).

110 R \*- S C (IN REP. 3).

131 AL -> V (IN REP. 3).

5315 GALBR \*- A PC (IN REP. 3).

5315 GALBR \*- A PC (IN REP. 3). US-08-468-011A-2.rsp \* (POTESTIAL).
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CYTODIASHIC (POTESTIAL). 3 (POTENTIAL). CYTOPLASMIC (POTENTIAL). Tue Nov 24 08:11:00 1998 CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT SEQUENCE 

2.2%; Score 12; DB 1; Length 466;

Query Match

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FT CARBOHYD 292 292 POTENTIAL. SQ SEQUENCE 459 AA; 52057 MM; F642C98E CRC32;

Query Match 2.4%; Score 13; DB 1; Length 459; Best Local Similarity 100:04; Pred. No. 5.784-16; Ddels Marches 13; Conservative 0; Hismatches 0; Indels 

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0; Indels 0;

01.40V.1995 (REL. 32, CREATED) 01.40V.1995 (REL. 12, LAST SECUENCE UPDATE) 02.40V.1997 (REL. 35, LAST ARROTATION UPDATE) GASTRIC THREBITORY FOURPETIDE RECEPTOR RECUSSOR (GIP-R) (GLUCOSE-DESTRAIN INSULINOTROPIC PALTERIA

MESOCRICETUS AURATUS (GOLDEN HAMSTER). EUKANUOTA, HETALOA, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA, RODSWITA.

RN 1520ENCE FROM N.A.

NEXULAR: 9511027.

M. MEDLINE: 1878. COMPAN Y., KUBOTA A., SEINO S., SEINO Y.,

M. MEDLINE: 1878. COMPANIOR. 25511561562192.

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A -> T (IN REF. 1).

R -> H (IN REF. 1 AND 3).

G -> A (IN REF. 1 AND 3).

H; C4AB952D CRC32;
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CYTOPLASHIC (POTENTIAL).
POTENTIAL.
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Score 9: DB 1; Length 438; Pred. No. 4.61e-05; 0: Mismatches 0; Indels Overy Match Best Local Similarity 100.0%; Matches 9; Conservative

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REAL STATE THE STATE OF THE REPORT FOR GLUGACOS-LIKE PETILE I. THE

C. I. FUNCTION: THESE IS A RECEPTOR FOR GLUGACOS-LIKE PETILE I. THE

ACTIVATE ADENIELL CYCLASE.

C. I. SUBCELLAND LOCATION: INTEGRAL MERBANE POPIENS WHICH

C. I. SUBCELLAND CACALIDE.

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RESIDE. PSOUGS, C. PROTEIN RECEP. P. 2.1 I.

RESIDE. PSOUGS, C. PROTEIN RECEP. P. 2.2 I.

RESIDE. PSOUGS, C. PROTEIN RECEP. P. 2.2 I.

RESIDE. STATE SOUGS, C. PROTEIN RECEP.

PROSITE FSOUGS, C. PROTEIN RE

PRT; RESULT 21 ID GLPR\_RAT STANDARD; AC P32301; Q64073;

Tue Nov 24 08:11:00 1998

RESULT 22

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RESULT 24

RE 413201996682.

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RE 413201996682.

RE 51 LAST SHERRED SHARED S

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Query Match 17%; Score 9; DB 1; Length 463;
Bert Local Similarity 100:0%; Pred. No. 4:64-05;
Marches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

Page 51

Tue Nov 24 08:11:00 1998

US-08-468-011A-2.rsp

Page 52

SEQUENCE PROM N.A.
SEQUENCE PROM N.A.
MEDLINE, 95145713.
WEI Y., MOJSOV S.;
PEBS LETT. 358:219-224(1995).

Page 50

US-08-468-011A-2.rsp

Tue Nov 24 08:11:00 1998

Page 49

01-0CT-1993 (REL. 27, CARATED) 01-0CT-1993 (REL. 25, LAST SECURNE UDDATE) 01-0CT-1997 (REL. 25, LAST ANNOTATION UDDATE) GLUCANOW-LIKE PEPTIDE I RECEPTOR PRECURSOR (GLP-1 RECEPTOR) (GLP-1-R). RATTUS NO GLER. RATTUS NONVESICUS (RAT). ESTINARYOM, RATELOM, CHORDATA, VERTERBATA, TETRAPODA, NAMMALIA; ESTINARYOM, RATELOM,

SEQUENCE FROM N.A.
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SEQUENCE THIS SEQUENCE ALL ISLEES,
MEDLINE: 24405572.
FROM SEC. NET. ACAD. SCI. U.S.A. 69:8641-8645(1992).

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PITERIAL ADENTATE CTCLASE ACTIVATING POLIFORPIDE TYPE I RECEPOR.
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CTODIASHIC (POTERTIAL).
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CLE_MOUSE STANDARD; PRT; 485 AA.

C 06.1804-1997 (REL_ 15, CREATED)

T 01-NOV-1997 (REL_ 15, LAST ANNOTATION UPDATE)

T 01-NOV-1997 (REL_ 15, LAST ANNOTATION UPDATE)

T 01-NOV-1997 (REL_ 15, LAST ANNOTATION UPDATE)

T 02-NOV-1997 (REL_ 15, LAST ANNOTATION UPDATE)
            TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-468-011A-2.xsp
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HEDLINE, 93206096.
JELINER L.J., LOK S., GRANT P.J., ROSENBERG G.B., SMITH R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ocery Match 17%; Score 9; DB 1; Length 468; Best Local Similarity 100:04; Pred. 100, 4: 616-05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                             2 (POTENTIAL)

EXTRACELLILAR (POTENTIAL)

3 (POTENTIAL)

4 (POTENTIAL)

EXTRACELULIAR (POTENTIAL)

5 (POTENTIAL)

6 (POTENTIAL)
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6 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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POTENTIAL
W: 718877DE CRC32:
                                                                                                                                 RECEPTOR;
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183 LFVSFMLRA 191
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RM 12.2

RM 5.2

RM 5
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TO PACE JURIAN STANDARD; PRI; 468 AA.

TO 1807-1995 (REL. 32, CREATED)

TO 1807-1995 (REL. 13, LAST SECURICE UPDATE)

TO 1807-1995 (REL. 13, LAST SECURICE UPDATE)

TO 1807-1995 (REL. 13, LAST SECURICE UPDATE)

DE PITULIANY ADMINIATE CYCLASA ANNINATING POLITEPTIDE TYPE I RECEPTOR

ON STRUKAROTA: WITHTAGA; CHORDATA, VERTERRATA: TETRAPODA, MAMMALIA:

RECURRENCY: PRITAGA; CHORDATA, VERTERRATA: TETRAPODA, MAMMALIA:

RA SECURICE FROM N. A.

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RA DICKERS: 4007199 (RECEPTOR 15, 1511-152) (1993)

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MUDLIE: 9331186.
SYGGON M. CICCARELLI E., TASTENOY M., CAUVIN A., STIEVENART M.,
EINCHEMS BOPHES. RES. COMMUN. 191:479-486(1991).
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KUIDPRO J.L., BIGGS S.H., WALKER K.M., CHEN L.H., MCKERNAN P.A.,
KINSYOGEL W.;
SCIENCE 259:1614-1616(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-468-011A-2.rsp
                                                                                                                                                                                                                                                  0; Indels
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1.7%; Score 9; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 4.618-05;
Matches 9; Conservative 0; Mismatches 0; Indels
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EXTRACELLUIAR (POTENTIAL).

S (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

6 (POTENTIAL).
FT CONFLICT 151 151 G -> A (IN REF. 1).
FT CONFLICT 221 221 G -> L (IN REF. 5).
FT CONFLICT 280 280 F -> L (IN REF. 1).
FT CONFLICT 289 289 F -> L (IN REF. 1).
FT CONFLICT 316 316 A -> G (IN REF. 2).
SQ SEQUENCE 461 AA, 53059 MM; 3D389103 CRC12;
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||172 LHCTRNYIH 180
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AND HEARTT. BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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CONTROL 5800850 CONTROL RECEP_72_1, 1
FROSTIE: PROMESSO CONTROL RECEPTOR CONTROL SIGNAL.
CONTROL TRANSMERSBANKS: GLYCOPROTEIN; SIGNAL.
CHAIN 27 485
GLACAGON RECEPTOR.
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RESULT 26
ID PACAGOSE STANDARD; PRT; 496 AA.
AC 970205;
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 170 LHCTRNYIH 178 |||||||||| 172 LHCTRNYIH 180

Tue Nov 24 08:11:00 1998

Best Local Similarity 100.0%; Pred. No. 4.61e-05; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

192 LPVSFMLRA 200 |||||||||||||| 183 LPVSFMLRA 191

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REALINE STATEMENT T. MEANTA T., OWINK I., OWIN H., N. MEDINE STATEMENT T. MEANTA T., OWINK I., OWIN H., N. MEDINE STATEMENT T. MEANTA T., OWINK I., OWIN H., N. MEDINE STATEMENT T. MEANTA T., OWING DEFECUT. 27

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Page 59

Tue Nov 24 08:11:00 1998

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ETINOSCELLILAR. (POTENTIAL).
S. (POTENTIAL).
CUDDALSHIC. (POTENTIAL).
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Query Match 1.7%; Score 9; DB 1; Length 513; Best Local Similarity 100:0%; Pred. No. 4:61-05; Mest Local S; Conservative 0; Mismatches 0; Indels Metches 5; Conservative 0; Mismatches 0; Indels Metches 0; Mismatches 0; Mism

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SURPRE FROM N.A. TISGURPE PROMICES; MEDLINE: 9331769 MEN S.A. PIESCHA J.R.; PROC. NRT. ACAD. 9CI. U.S.A. 90:5345-6349(1993).

TISGUES PRAIM:
TREADLES: 93126107
REGORA M., ORDA M., OGI K., MASUDA Y., MIYAMOTO Y., OHTAKI T.,
FORLARK H., ALENDARA A., FORLING M., PARIS A.
SCOREM. ELORHES. RES. CORMON. 194:133-143(1993).

Page 58

Tue Nov 24 08:11:00 1998

Page 57

US-08-468-011A-2.rsp

PITUITARY ADENYLAIE CYCLASE ACTIVATING POLYPEPTIDE TYPE I RECEPTOR PRECESSOR (PACAP TYPE I RECEPTOR) (PACAP-R-1). ACCYADIRI. S'MUSCULUS (MOUSE). KARNOTA, PETILOD: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA: THERIX; RODENTA.

THE SECURATE FROM N.A.

MASTILLON CHARACTOR M., HAGIGARA N., OGAWA N., NISHINO A.,

MASTILLON CHARACTOR M., HAGIGARA N., OGAWA N., NISHINO A.,

MASTILLON CHARACTOR M., PANCHARA M., PANCHARA M.,

MASTILLON CHARACTOR M., PANCHARA M., PANCHARA M.,

MASTILLON CHARACTOR M., PANCHARA M., PANCHARA M.,

A ROCHILLIT CALCARE N.A. RECULARE N. PROCEPTION WILLIAM ACTIVATE OF CALCARETIN MINERAL M. PROCEPTION WILLIAM CALCARION. THE RELAXATION AND SECRETION IN THE CASTORIATE M. PANCHARA M. PREMAMENTOR M. PANCHARA M. PANC

POTENTIAL (BY SIMILARITY).
PIUTINARA MORENARE CYCLASE
POLYEPPINE TYPE I RECEPTOR.
EXTRACLILLIAR (POTENTIAL).
CYTOPIASHIC (POTENTIAL).
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SUPPREMIALA.
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POTENTIAL). OTENTIAL. B3C914FE CRC32; 60 PO 117 PO 56639 MW;

1.7%; Score 9; DB 1; Length 496

Query Match

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EXTRACELLULAR (POTENTIAL)

POTENTIAL.
MISSING (IN SHORT FORM).
, OE9E59B1 CRC32;

209 LEVSPHIRA 217 ||||||||| 183 LEVSPHIRA 191

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PRICE 25.
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SEQUENCE FROM N.A.

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RESIDENCE FOR S. LE RALMANIN N. E., FOSTER D.N. S.

RESIDENCE FOR S. LE RALMANIN N. E., FOSTER D.N. S.

C. 1- FOSTER FOR S. MEDIATED BY G. PROTEINS WHICH ACTIVATE ADENTLY.

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CTYOPLASHIC (POTENTIAL).
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MISSING (IN HOP2).
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1.74: Score 9; DB 1: Length 523;
Best Local Similarity 100.04; Pred. No. 4.61e-05;
Matches 9; Conservative 0; Mismatches 0; Indela
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EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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4 (POTENTIAL).
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255 LVEGLYTH 262
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SEQUENCE
      Page 61
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US-08-468-011A-2.rsp
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SEQUENCE FROM N.A.
HEDLINE; 9338265.
SEERINE P. . JOHNNET C., PANTALONI C., HOLSBOER P., BOCKAERT J.
MATURE 365:170-175 (1993).
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TISSUE-SIGNITANY:
MEDLINE: 93351025.
MEDLINE: SISTHAMA T., SHIGEMOTO R., MORI K., MAGATA S.;
MEDRON 11:333-43(1933).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EBÖGIENCE PROM N.A.
PERLINE: 93359078. TISSUE-OLRACTORY BULB;
MEDLINE: 93359078. M., WEST K.M., FINK G., HARMAR A.J.;
FEBS LETT: 323:99-105(1993).
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1.5%; Score 8; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.050-02;
Matches 8; Conservative 0; Mimmatches 0; Indels
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449 GSVLTTVT 456
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AND ESCOUR E.B.:

IN PROCRINGOUS 133:72-77(1896).

IN PROJECT 133:72-77(1896).

IN PROCRINGOUS 133:72-77(1896).

IN PROJECT 133:72-77(1896).

IN PROCRINGOUS 133:72-77(1896).

IN PROSITE; PROCRIA PRINTY OF MILKY A DOFFUTAL CYCLASE.

IN PROSITE; PROCRIA PROCRIA PROPER.

IN SELONGE OF PROTEIN RECEP 2-1.1.

IN PROSITE; PROCRIA OF PARINY ENCEP 2-1.3.

IN PROSITE; PROCRIA OF PARINY ENCEP 2-1.3.

IN PROSITE; PROCRIA DE PROFESSE P.2.3.

IN PROSITE; PROCRIA P.2.3.

IN PROSITE; PROCRIA PROFESSE P.2.3.

IN PROSITE; PROCRIA PROFESSE P.2.3.

IN PROSITE; PROCRIA PROFESSE P.2.3.

IN PROFESSE PROFESSE P.3.

IN PROSITE; PROCRIA PROFESSE P.2.3.

IN PROFESSE PROFESSE P.3.

IN PROFESSE PROFESSE PROFESSE P.3.

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IN PROFESSE P.3.

IN PROFESSE PROFESSE P.3.

IN PR HOMO SAPTENS (HUMAN). SKRANYCHA: MEMZAGA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA. EUTHERIA: PEIMATES: 

EXTRACELLUIAR (POTENTIAL).
1 (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
CTOPLASHIC (POTENTIAL).
CTOPLASHIC (POTENTIAL).
CTOPLASHIC (POTENTIAL). 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL). 5 (POTENTIAL).

(POTENTIAL). POTENTIAL. POTENTIAL. 9158074E CRC32;

Query Match 1.5%, Score 8: DB 1; Length 411; Beatcheas Similarity 100:09; Pred. No. 1.05-02; Indels Matches 9: Conservative 0; Mismatches 0; Indels Mismatches 0.

HACELLUIAR (POTENTIAL). POTENTIAL).

Page 67

Tue Nov 24 08:11:00 1998

Page 68

US-08-468-011A-2.rsp

THE STATEMENT PROM N.A.

THE STATEMENT PROM N. 

349 SPOGPEVS 356 ||||||||| 403 SPOGPEVS 410

US-08-468-011A-2.rsp

Tue Nov 24 08:11:00 1998

PLANT MOL. BIOL. 20:481-491(1992).
EMILIANTY BELONGS TO PEPTIDAE FAMILY US.
EMEL, XASO49, 0.3965; .
PROPERIELAL PROTEIN: HYDROLASE; SERINE PROTEASE.
NOW.TER 411 411 411 415 45418 NM; 95A71CF2 CRC32;

Query March 1.5%; Score 8; DB 1; Length 411; Best Local Similarity 100:09; Pred. 180. 1.056-02; Marches 8; Conservative 0; Mismatches 0; Indels March

15 LVLVLVPG 22 ||||||||| 366 LVLVLVPG 373

THE STRAIGHT OF THE CAN, CRICORADIS D.E., CLEVENGER W.,

AN CHEMBRICA T.W., LIAM C.M., CRICORADIS D.E., CLEVENGER W.,

AN CHEMBRICA T.W. DE DOLLA E.B. OLTERSONE T. 1959.

CH. THORTON. THE ST. A REPERPOR PRO CONTINCENDENT RELEASING PATCHS.

SHOWS HIGH-APPRINT CAP SHIDING. THE ACTUTY OF THIS RECEPORS IS

CH. THORTON. THE ST. A REPERPOR PRO CONTINCENDENT COLLARS. THE RAIN ORDER OF DOPTENY FOR THIS RECEPORS IS

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CH. STREELLAAL COLLING INTEGRAL MEMBRARE PROTEIN.

CH. STREELLAAL COLLING INTEGRAL MEMBRARE PROTEIN.

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CH. ALSO DISTINGED THE SEPTOM AND CRESS THE SEPTOM AND CR RESULT 32

10 CREP\_LANT STANDARD: PRT: 411 AA.

11 CREP\_LANT

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14 TO 15 CREP\_18 CREATED

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The Row 24 08:11:00 1998  The Supplement From R.A.  RESIDENCE FROM RELEASING FACTOR.  RESIDENCE FROM RESIDENCE FROM RESIDENCE FACTOR.  RESIDENCE FROM RELEASING FACTOR.  RESIDENCE FROM RESIDENCE FROM RESIDENCE FACTOR.  RESIDENCE FROM RELEASING FACTOR.  RESIDENCE FACTO	The Nov 24 08:11:00 1998  FT CARBOHD 55 95 POTEBTAL.  SO SCHOOL 157 100.03: PRESTILE CROSS CONTINUED CONTI
69 66 64	Page 71.
The Nov 24 08:111:00 1998  The Nov 24 08:111:00 1998  The Cornels of Condition of C	The Mov 24 09:111:09 1999  Db 333 SPOGFPW 500  V 403 SPOGFPW 510  Oy 403 SPOGFPW 510  Oy 403 SPOGFPW 510  MEEULA.  A SPOGFPW 510  O CONTROLLED CHICKERS STANDARD; PRT; 420 AA.  A SPOGFPW 510  O CONTROLLED CHICKERS STANDARD; PRT; 420 AA.  A SPOGFPW 510  O CONTROLLED CHICKERS STANDARD; PRT; 420 AA.  AN MEDILLED SALLES

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Page 74
                             01-FEB-1994 (REL. 28) LAST SEQUENCE UPDATE)
01-ROW-1997 (REL. 18). LAST ANNONTION UPDATE)
008TGOTROPH RELEASING FACTOR RECEPTOR 1 PRECURSOR (CRF-R) (CRF1).
CRR 10 RELR OR CRF.
CRR 10 CRF RIN OR CRF.
EUGHNOOR SAFIERS (HUDAR).
EUGHNOOR METALOCA (HORDAIN, VERTEBRAIN, TETRAPODA, MARALLIA;
EUGHNETAL, PRIANTES.
                                                                                                                                                     LATOURNEE FROM N.A.
TISSUE-BRAINTH;
VITA.N., LAUGENT P., LEPORT S., CHALON P., LELIAS J.-M., KAGHAD M.,
LE FUN G., CAPUT D., PERRARA P.;
LE FUN G., CAPUT D., PERRARA P.;
US-08-468-011A-2.rsp
                                                                                                                     MEDLINE; 94022296.
CHEN R., LEWIS K.A., PERRIN M.H., VALE W.W.;
PROC. NATL. ACAD. SCI. U.S.A. 90:8987-8971(1993).
Tue Nov 24 08:11:00 1998
                               Page 73
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PRT;
                                               RESULT 38
ID CREK_HUMAN STANDARD;
AC P14998; Q13008;
DT 01-FEB-1994 (REL. 28, CREATED)
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0; Indels

Query Match 1.5; Score 8; DB 1; Length 431; Best Local Similarity 100;00; Pred. No. 1.05-02; Peredres 0; Indels West-these 9; Conservative 0; Mismatches 0; Indels

POTENTIAL:
POTENTIAL:
POTENTIAL:
POTENTIAL:
POTENTIAL:
POTENTIAL:
PO < >> OOI (IN REF. 2).
RX -> NG (IN REF. 3).
RX -> NG (IN REF. 3).
A -> SG (IN REF. 2).
4743352E CRC12.

CORTICOTROPIN RELEASING PACTOR RECEPTOR US-08-468-011A-2.rsp EXTRACELLULAR (POTENTIAL).
CTOPLASHIG (POTENTIAL).
CTOPLASHIG (POTENTIAL).
A (POTENTIAL).
S (POTENTIAL).
CTOPLASHIG (POTENTIAL).
CTOPLASHIG (POTENTIAL). (POTENTIAL).

(POTENTIAL).

(POTENTIAL).

TOPIASMIC (POTENTIAL).

TENTIAL.

OTENTIAL. EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CTOPLASHIC (POTENTIAL).
2 (POTENTIAL). (POTENTIAL). Tue Nov 24 08:11:00 1998 CHAIN

Query March 1.5%; Score 8; DB 1; Length 444; Best Local Similarity 100.08; Pred. No. 1.056-02; Marches 8; Conservative 0; Mismarches 0; Indels Marches 9; Conservative 0; Mismarches 0 g

GLOCKASTOLIGICAPRSPAGGLVVRDCPAFFYGVRINTTN
-5 D (IN CRF.R3).
-SESTOR (IN CRF.R3 AND CRF.R3).
CAERCO3C CRC12; 146 174 Mi 444 AA; 50719 MW; VARSPLIC SEQUENCE TRANSEM DOMA IN TRANSEM DOMA IN TRANSEM DOMA IN TRANSEM DOMA IN TRANSEM TRANSEM DOMA IN TRANSEM TRANSEM ORMA IN TRANSEM CARBORTO 
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Page 75

ESTORMER FROM N.A.
STRAINSOROF / ABOYZ
STRAINSOROF / ABOYZ
STRAINSOROF / ABOYZ
STRAINSOROF / ABOYZ
AVILES E. DERNO A. THERINAN T. CARPENTED, T. CHERR E. CHERRY T. H.
AVILES E. DERNO A. THERINAN T. CARPENTED, T. CHER T. H.
HTAN R. KAYER M. A. CODA C. LARMINALD, L. HRYLEF-SHITH S. T.
HTAN R. KAYER M. A. KODP C. LARMINAL D. THE M. LIN D.
PETEL P. A. KODP C. LARMINAN A. SCHAMAR A. SCHAMER P. OBENER P. OBENER P. SELLO P. NAKHANA M. SCHAMAR D. SCHAMAR D. SOURHITH D. DAYS ROPER P. SELLO P. M. POTETZIN D. DAYS R. STRAIN V. SUTTHIN V. SUTHIN TO SUTHIFINED TO SUPPLIE TO SUPPL MOL. MICROBIOL. 4:585-596(1990). [2] Tue Nov 24 08:11:00 1998

BRAIN

1- STRILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

EMEL: 011293 0372355.

EMEL: 013939, 0406744.

PROSITE: PROOF691 C\_PROTEIN RECEP\_F2\_1: 1.

PROSITE: PROOF691 C\_PROTEIN RECEP\_F2\_2: 1.

PROSITE: PROOF691 C\_PROTEIN RECEP\_F2\_2: 1.

RECEPTOR TRUNKERSHARE; GITCOPROTEIN; SIGNAL.

SIGNAL

CHAIN 25 431 CORTICOTROPIN RELEASING PACTOR RECEPTOR

EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL). POTENTIAL) TRANSPER DOMAIN TRANSPER TRANSPER DOMAIN TRANSPER TRANSPER DOMAIN TRANSPER DOMAIN CARBORED CA

TOPLASMIC (POTENTIAL).
(POTENTIAL).
(TRACELLUIAR (POTENTIAL).
(POTENTIAL).
(TOPLASMIC (POTENTIAL).

SLLULAR (POTENTIAL) 6 (POTENTIAL) EXTRACELLUIAR (POTENTIAL).

POTENTIAL).
OPLASHIC (POTENTIAL).
ENTIAL.

POTENTIAL). POTENTIAL).

Tue Nov 24 08:11:00 1998

US-08-468-011A-2.rsp

JENCE PROM N.A. (CRP-R3). SUE\*HIPPOCAMPUS;

TANGENGE AND THE PROCESSION OF THE STATE OF

US-08-468-011A-2.rsp

Page 76

SECUENCE OF 380-533 FROM N.A. MEDLINE, 91161150. THERBUSCH A.G., PING.R.; J. BIOL. CHEM. 258:5238-5247(1983).

Indels Query Match 15%; Score 8; DB 1; Length 533; Bef Local Similarity 100.0%; Pred. No. 1.05e-02; Matches 8; Conservative 0; Mismatches 0; Indels

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Page 80
             Page 78
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PROSITES, PROBLES, OSTOLIDS, PERCURSOR. 1.
CRANKING ON PARE DASIC RESIDUES; SIGNAL, ENDORPHIN, NEUROPEPTIDE; OSTOLID PEPTIDE. OF DASIC RESIDUES; SIGNAL, ENDORPHIN, NEUROPEPTIDE; SIGNAL PEPTINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SÉCIENCE PROM N.A.
HEDLINE: 95000136; PROM N.A.
HEDLINE: 95000136; PROPENDE CLAND;
BENCHIEN: 95000136; PROPENDE M.: DESCROSZILLERS L., BRAKIER-GINGRAS L.;
BENCHIEN: 131:931-940(1994);
-1- FTM: THE N-TERRIAL CONTAINS 6. CONSERVED CYSTEINES THOUGHT TO
BINNOLVED IN DISCURLE BONDING AND/OF PROCESSING.
-1- SIMILARIT: BELONGS TO THE OPIDIDS NEUROPEPILDES PRECHESORS
-1- MAILLY.
                                                                                                                                                      CC -1- SUBCELLUTAR (LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

PROTEIN: 184 201-185.

PROTEIN: 184 201-185.

PROTEIN: 184 201-185.

PROTEIN: 184 201-185.

PROSENEM: 18 9 POTENTIAL.

PROSENEM: 139 159 POTENTIAL.

POTENTIAL.

SQ SEQUENCE 178 AM: 20160 MM: B1407893 CRC32;
      US-08-468-011A-2.rsp
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Matches 7; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 VGYSISP 159
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|||||||
Qy 207 VKELESL 213
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      Tue Nov 24 08:11:00 1998
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ID RL6_CAEEL
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Page 77
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BACHLUS SUBTILLS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACHLIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACILLUS SUBTILIS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
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NOTE AND THE STANDARD: PRT; 178 AA.

NOTE AND THE A
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DIT OLYEN-1996 (REL. 3), CREATED)

DIT OLYEN-1996 (REL. 3), LAST SECURED UPDATE)

DIT OLYEN-1996 (REL. 3), LAST ANNORMATION OF DATE

DIT OLYEN-1996 (REL. 3), LAST ANNORMATION OF DATE

DIT OLYEN-1996 (REL. 3), LAST ANNORMATION OF DATE

CREATED 1996 (REL. 3), LAST ANNORMATION OF DATE

CREATED 1996 (REL. 3), LAST ANNORMATION OF DATE

CREATED 1996 (REL. 3), TO ENGLORATES; REMATION; SECRETERING, RANDITIDA.

REPORTING (REL. 1997) TO ENGLORATES; REMATINY OF REDGGOMAL PROTEINS:

CREATED 13, CREOTO, CREATED 13, CREOTO, 4.

DR PROSITE; PROFEIN:

REPORTING 1991 (AND STORE) REMATING OF REDGGOMAL PROTEINS:

DR PROSITE; PROFEIN:

REPORTING 1996 (AND STORE) REMATING OF REDGGOMAL PROTEINS:

SEQUENCE 217 AA), 24313 MM; ALAGESTOR CRC22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels 0; Gaps
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EURARYOTA: METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
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SPRAIN-168 OF VHIATO
KORNIASHI T., MIZUOO M., MASUDA S., TAKEMARU K., HOSONO S.,
TOTT, TAKEOTHI HI, SPREEL/GENBANK/DDBJ DATA BANKS.
SUBMITTEEL (MKI-1985) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.3%; Score 7; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.41e+00;
Matches 7; Conservative 0; Mismatches 0; Indels
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VIRIDAE: DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE.
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10 V57B_BP74 STANDARD, PRI, 153 AA.

(C P05733; FREL 05, CREATED)

T 13-AGC-1987 (REL 05, LAST SEGOUNCE UPDATE)

T 01-FEB-1995 (REL 01, LAST ANDOTATION UPDATE)

E GREES 57B PROTEIN (PROTEIN GP57B).
                                                                                                                                                                                                      133 LIFVAFFS 140
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264 LIFVAFFS 271
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| | | | | | | |
Qy 320 APILAAI 326
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      Tue Nov 24 08:11:00 1998
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Page 84
            Page 82
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PROKANCA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS
SPYEROBACTERACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SÉGUBNCE FROM N.A.
STRAINHEAT / MOISÉST
STRAINHEAT F. R., PLUNKET G. III, MAYHEM G.F., PERNA N.T., GLASHER F.D.,
SCHRITTED (JAN-1997) TO EMEL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUCENCE FROM N.A.
TISSUED-818.6
RESULP-816186.
ROWELLS B.D. KILPATRICK D.L., BHATT R., MONAHAN J.J., POONIAN M., PROC. NATL. ACAD. SCI. U.S.A. 81:7651-7655(1984).
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KREIL M. KASHIMOTO K. IISONO G. ITOM T. KANLI K.,
KREIL H. KASHIMOTO K. INI S. KUUDA S. KITAGAM A. K.
KROIL M. KASHIMOTO K., KANSHIMOTO S., MIKI T., HIZOUCHI K., MORI H.,
KOTOMIRA K., MAKMURA Y., MASHIMOTO H., MISHIO T.,
SANDONI M. SAMPEL G., SEKI I. Y., TAGMI H.,
KRAMANOTO T., TAND M.
SUBMITTED (DEC-1986) TO EREL/GENBARK/DDBJ DATA BANKS.
      US-08-468-011A-2.rsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RATTOS NONVECICOS (RAT).
ESTRANTOTA, HETALOA, CHORDATA; VERTEBRATA; TETRAPODA; HAMMALIA
EQTHERLA, RODERTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.3%; Score 7; DB 1; Length 269; Best Local Similarity 100.0%; Pred. No. 1.41e+00; Matches 7; Conservative 0; Mismatches 0; Indels Matches 1; Conservative 0; Mismatches 0; Indels
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ROSEN H., DOUGLASS J., HERBERT E.; J. BIOL. CHEM. 259:14309-14313(1984).

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15 ORAWATCIS POLYCREDIS STRANDAR STREPOWICETACEAE.

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Schneider, J. Pharmacol. (1993) 246:149-155 Cloning and functional expression of a human parathyroid
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Journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:8641-8645

Fille Expression closing of the pencreatic beta call receptor for the glucon-increase and processing the gluco-incretin hormone glucagon-like peptide 1.

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ö Wei, Y.; Mojsov, S. P. 129-224 PERS Lett. (1995) 156-219-224 Tissue-specific expression of the human receptor for glucagon-like peptide-1; brain, heart and pencretic forms syl624 has akene deduced amino acid sequences. vipy receptor. hume from septent of formal lane from septens from 06.5un-1997 frext\_change 06.5un-1997 Ouery Match 1.7%; Score 9; DB 2; Length 463; Bet Local Similarity 100.0%; Pred. No. 4:58c-04; Marchea 9; Conservative 0; Mismatchea 0; Indela 0; Gaps 871624 stype complete
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Bengier, D.; Waeber, C.; Pantaloni, C.; Holaboer, F.; Bockert, J.; Seeburg, P.H.; Journot, L.
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Spine ARAP receptor.
Hosoya, M.; Onda, M.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Oktakik, M.; Arimara, A.; Pulino, M. Biochem. Biophys. Res. Commun. (1993) 194:133-141 Moltecular Cloning and functional expression of rat cDkna encoding the receptor for pituitary adenylate cyclase ectivating polypeptide (PACAP).
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#length 467 #molecular-weight 53232 #checksum 4520 SUMMARY

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FRENCE Tigists: Thorret, A.: Buehler, L.; Deng, S.: Morel, P.: Wathbors Thornan, B.: Porret, A.: Buehler, L.; Deng, S.: Morel, P.: Widmann Disheres (1991) 42:1678-168 and functional expression of the human islet GLP-1 receptor. Demonstration that exendin-4 is an agonist and excession of the receptor.

Federate preliminary; translated from GB/EMEL/DOBJ steplentle-type mRNA 
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#domain transmembrane #status predicted #label TMIN #domain transmembrane #status predicted #label TMIN #domain transmembrane #status predicted #label TMIN #domain transmembrane #status predicted #label TMIN #domain transmembrane #status predicted #label TMIN #domain transmembrane #status predicted #label TMIN #domain transmembrane #status predicted #label TMIN #domain transmembrane #status predicted #label TMIN #domain transmembrane #status predicted #label TMIN #domain transmembrane #status predicted #label TMIN #l

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#binding\_site carbohydrate (Asn) (covalent) #status predicted #length 485 #molecular-veight 54872 #checksum 5999

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S39063 #type complete pituitary adenylyl cyclase activating-peptide receptor form 5

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picegna, J.R.; Mank, S.A. (1993) 90:5145-6349 Molecular cloning and functional expression of the pituitary definite cyclass-activating polypeptide type I receptor. A43204

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RESULT 32 ENTRY TITLE

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Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Frankai, M.; Levine, P.; Lesias, J.M.; Frankai, M.; Perrars, P.; Prins, Levi. (1999) 353:1-5 cart. (1995) 4 cart. (1
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\*\*residues 1-191'/M',193-260'/G',262-533 \*\*label WEB ecross \*\*reference EMBL/ST51; NII:93699; PID:93700 \*\*experimental\_cource strain Filo

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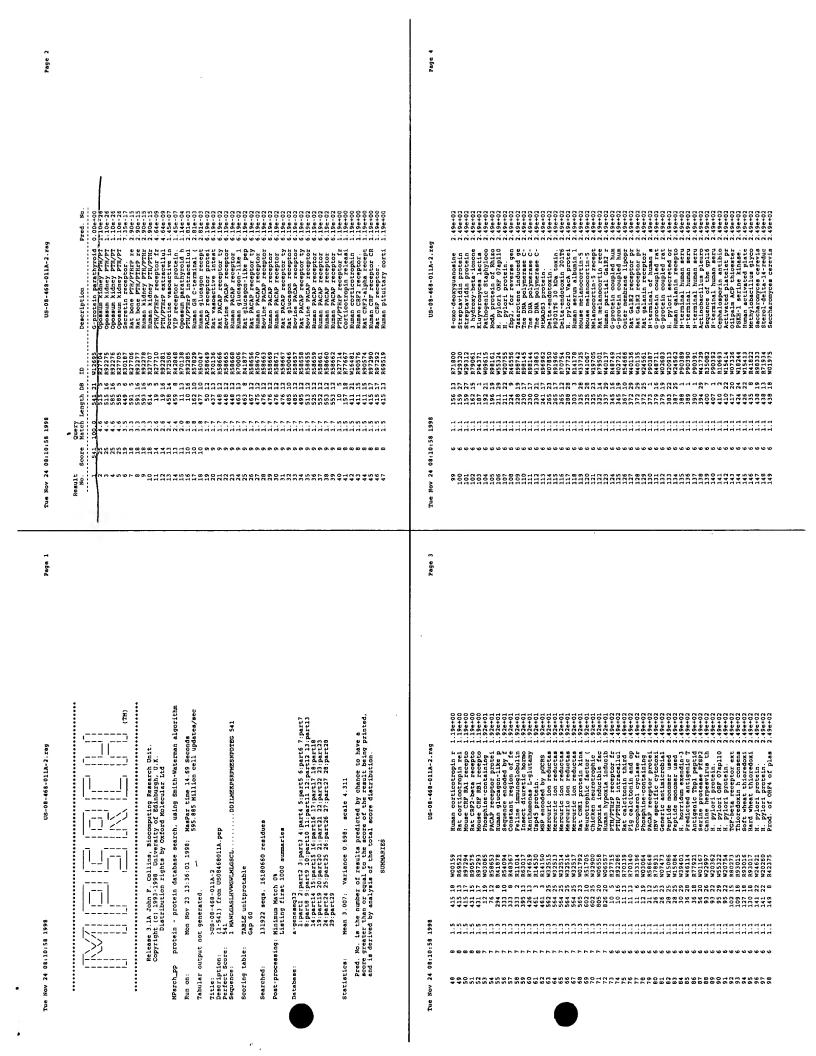
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Class 1. Fig 3A-2E. 64pp; English.

Parathyroid homone/parathyroid homone-related protein (PTH/PTHP)

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Fig. CLI expressing the recens for (ant) agonists and to raise antibodies.

Sequence SSS AN;
                                                                                        DNA encoding vertebrate parathyroid hormone receptor - useful for disposals and treatment of e.g. hypercaleaemia, hypo-caleaemia, cancer etc.
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0; Mismatches 0; Indels
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R92276 standard; Protein; 585 AA.
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Ouery Match 4.6%; Score 25; DB 16; Length 585; Best Local Similarity 10.0%; Pred No. 1.10e-26; Indels 9; Caps Marches 25; Conservative 0; Minmarches 9; Indels 0; Caps

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/note= "potential N-glycosylation site"
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//note- *potential N-glycosylation site*
//note- *potential N-glycosylation site*
//note- *potential N-glycosylation site*
                /note= "signal peptide"
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Page 27

secretin receptor protein encoded by this gene may be used in basic research and in clinical tests, and is available in high yield. Sequence 449 AA; Ouery Match 3.5%; Score 19; DB 6; Length 449; Beet Local Similarity 100.0%; Pred. No. 7.35e-17; Matches 19; Conservative 0; Mismatches 0; Indela

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TO RE2706;

DE RATOGE standard: Protein; 591 AA.

DE RATOGE.

DE RATE DONE PRIVETE RECEPTOR CLONE RISE Prod.

Rate DONE PRIVINGIA MORDING: Felated protein; calcium; antagonist;

MA BARANIVOIR MORDING: Related protein; calcium; antagonist;

MA ARTIDOIRES ARTIDOIRES ARTIGE.

DE RATE-1993; 002831.

PR 05-ARF-1993; 002831.

PR 05-ARF-1994; 002831.

PR 05-ARF-1

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Tue Nov 24 08:10:58 1998

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Page 26

The MARNEL STATE CONTRINGUE OF THE STATE OF RESULY.

DE RATIOS standard, Protein, 585 AA.

REAL RATIOS STANDARD STANDAR

Query Match Similarity 100.09, Pered. No. 1.10e-06; Length 585; Matches Local Similarity 100.09, Pered. No. 1.10e-06; Matches 25; Conservative 0; Mismatches 0. Indels 0; Gaps

Tue Nov 24 08:10:58 1998

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Gaps

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To coding for secretin receptor - is expressed in COS cells and produces a receptor protein for research and clinical use produces a receptor protein for research and clinical use. The accretin receptor was encoded by a DNA sequence of rat origin. Once accretin receptor was encoded by a DNA sequence of rat origin. Security of a constitued in rat/Bouse hybridoma NG108-15. The DNA sequence was obed. from a cDNA library derived from NG108-15 calls. Expression to a mitable host allows produ. of the receptor protein. The

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PD 07-PEB-1936.

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PD 07-PEB-1937.

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Gaps

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N: 151-6-159228-15
N: 151-6-15928-15
N: 151-US-08-468-011A-2.rag Query Match 3.31; Score 18; DB 16; Length 593; Best Local Similarity 100.08; Pred. No. 2.90e-15; Marches 18; Conservative 0; Minmatches 0; Indele M27707 and andard; Protein: 614 AA.
R27707 standard; Protein: 614 AA.
R27707 standard; Protein: 614 AA.
R27707 standard; France entry;
Ruman X.deny PTM/PTMP receptor.
Buran X.deny PTM/PTMP receptor.
Buran X.deny PTM/PTMP receptor.
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Contenting a human Kidney of human placental DNA in Employed and pure our prize and pure our prizery in labels as ground in the coding sequence of that bone parasity to probe comprising most of the coding sequence of that bone parasity copies comprising most of the coding sequence of that bone parasity receptor protection. The clone encodes a protein which may be used in a compression of parasity of the present of the present of the present of the compression of DNAs homoologue to PFIR DNAs can be identified using the protein produce of and DNAs homoologue to PFIR DNAs can be identified using the protein produce of one as protein DE MATION Standard: peptide: 19 AA.

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NESSULT. 13
FORCELOS STANDARDE STANDARD STANDARD STANDARD STANDARDE STANDARD STANDA ö Gaps Gaps Score 13; DB 14; Length 458; Pred. No. 1.45e-07; 0; Mismatches 0; Indels 0; Best Local Similarity 100.0%; Pred. No. 4.64e-09; Matches 14; Conservative 0; Mismatches 0; Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative 

US-08-468-011A-2.rag

Page 36

PS Discloure: Figure 3: 19pp: English.

CC VIP2 Lean adenylare organes—linked VIP receptor from rat brain. The VIP2 Lean adenylare organes—linked VIP receptor from rat brain. The VIP2 receptor was identified by PRC of rat pituitary CDNN using CV VIP2 receptor was identified by PRC of rat pituitary CDNN using CV VIP2 receptor of pituitary control organization of pituitary control organization of pituitary control organization of the rat pituitary of Grands of CV VIP2 receptor (NOTA). The secretin family of Grands of the rat exerctin, CV VIP2 receptor is expected from an opename parabyloid hormone (PNT) receptors (see PNT) 19pp. CV VIP2 receptor (see CV VIP2 receptor is a companied to probe comprising a labelled DNN or RNN sequence capable or specifically binding to a gene for VIP2 receptor is sequence.

Score 11; DB 13; Length 11; Pred. No. 1.14e-04; 0; Mismatches 0; Indels 0; Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative onare. Column 3: 64pp; English.
Parkhyroid hormone (PFH) receptor fragments, including those Parkhyroid hormone (PFH) receptor fragments, including those (1822)79-89. based on the Intracellular tespon and those (18228-87) based on the Intracellular domain, are produced by incorporating encoding DNA sequences into a vector, and

Page 34

US-08-468-011A-2.rag

99 lveglylhnl 108 ||||||||||| 255 LVEGLYLHNL 264

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Ouery Match
1.8%; Score 10; DB 10; Length 477;
Best Local Stmilarity 100.0%; Pred No. 2.88-0; Indels 0; Caps
Miches 0; Indels 0; Caps

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RESULT 19
1D R88649 standard; Peptide; 50 AA.
AC R88649,
DI 12-MAY-1955 (first entry)
DI RACAP receptor protein homology region 7.
KM Bowine; pitultary adenylate cyclase activating polypeptide; PACAP;

Tue Nov 24 08:10:58 1998

Page 39

183 LFVSFMLRA 191

US-08-468-011A-2.rag

Page 40

II 780 Standard, Protein, 437 AA.
R70156
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// /label= Potential glycosylation site 91

/label see above modified\_site peptide

peptide domain

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Page 37

culturing coils transformed by the vercor. The peptides can be used to ratio antibodies. The predictes are useful in the treatment, disgnosis or progness of e.g. hypercalcemia and the content of the co

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Score 10; DB 16; Length 10; Pred. No. 2.81e-03; 0; Mismatches 0; Indels 0; Gaps Query Match Bent Local Similarity 100.0%; Matches 10; Conservative

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1 frihetrny 10 ||||||||||| 169 FRRLHCTRNY 178

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PRESULT 117

TO 187292 crandard; Protein; 162 AA.

AC 87329.

AC 6771394 (fifter entry)

DE 18820 craft 1994 (fifter entry)

ENTRY human; glucagon receptor; transgenic animal; metaboliam; model;

RAT human; glucagon receptor; transgenic animal; metaboliam; model;

RAT 97407369.

PROME 1892 (G. 1891)

PROME 1892 (G. 1892)

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ery Match st Local Similarity 100.0%; tches 10; Conservative

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Score 10; DB 10; Length 162; Pred. No. 2.81e-03; 0; Mismatches 0; Indels 0;

Tue Nov 24 08:10:58 1998

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adenylate cyclane: receptor; type lh; signal sequence; hydrophobic cluster; framemembrane; human; PACAP receptor; pitutkary; \$\frac{1}{2}\text{Additionals}, diagnosis; neuropathy; Althelmer's disease; gene therapy; sorrecting; amony; neuropathy.

PR 2-F201-1394.

PR 2-F201-1394.

PR 2-F201-1394.

PR 2-F201-1394.

PR 2-F201-1395.

PR 17-ARR-1395. JP-131465.

PR 17-ARR-1395. JP-131465.

PR 17-ARR-1399. JP-131466.

PR 17-ARR-1399. JP-131466.

PR 17-ARR-1399. JP-13146.

PR 27-ARR-1399. 
PR 27-AR

26 lfvsfmlra 34

Query March 1.7%; Score 9; DB 12; Length 50; Bent Local Similarity 100.0%; Pred. No. 6.19e-02; Marches 9; Conservative 0; Minnatches 0. Indels

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0; Indels 0;

Tue Nov 24 08:10:58 1998

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Page 42

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Query Match 1.74, Score 9, DB 12; Length 448; Best Lone Similarity 100 04; Pred, No. 6.18e-02; Indels Matches 9; Conservative 0; Hismacches 0; Indels

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172 lfvsfmlra 180 | | | | | | | | | | | 183 LFVSFMLRA 191

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REBULT 5.

RESULT 5. 

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Page 43

US-08-468-011A-2.reg

Page 44

PR 26-FER-1991; JP-018753.

PR 77-ARR-1991; JP-018650.

PR 77-ARR-1991; JP-018660.

PR 77-ARR-1991; JP-018660.

PR 77-ARR-1991; JP-108660.

PR 77-ARR-1991; JR-10860.

PR 77-AR

Score 9; DB 12; Length 448; Pred. No. 6.19e-02; 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0%; Matches 9; Conservative 172 lfvsfmlra 180 g

Gaps

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183 LFVSFMLRA 191

RESULT 24 ID R70006 standard; Protein; 463 AA.

Page 41

on the third and eventh transmembrane domains of the rat secretion pig educationin and opossum parethyroid horsmone (PPH) receptors (see R70137-R70140. Pull length chins were lacked from an olfactory bulb colb. Library. The sequence has been submitted to the EMBL/GenBank detabase under accession No. 225895 (see 093211/R70136).

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ö Score 9; DB 13; Length 437; Pred. No. 6.19e-02; 0; Mismatches 0; Indels 0.00 Match Best Local Similarity 100.0%; Matches 9; Conservative

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Best Local Similarity 100.0%;
Matches 9; Conservative

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RESULT. 23

AD 185668 standard; Protein; 448 AA.

AD 58568. Standard; Protein; 448 AA.

AD 12-MAY-1995 (first entry)

BE Human PACAP receptor type IA, mature protein;

BOWING: Tat; pituitary adequiate syclass extivating polypeptide; PACAP;

MY Addroplood; cluster; transmembrane; human; ACAP receptor; pituitary;

MY Addroplood; cluster; transmembrane; human; ACAP receptor; pituitary;

MY Addroplood; cluster; transmembrane; human; ACAP receptor; pituitary;

MY STEP 61994; assay; neuropathy; Alsheimer's disease; gene therapy;

MY PE 61894.

PE 62694.

PE 62694; 102757.

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PF 905504811-A.

10-720-1995.

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10-7400
/label= N-linked glycosylation
modified_site 82
  modified_site 115
/note= see above*
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Ouery Match
1.71, Score 9, DB 13; Length 463;
Best Local Similarity 100,04, Pred, No. 6.13e-02;
Matches 9; Conservative 0; Minnatches 0; Indels 0; Gaps 172 lhctrnyih 180 172 LHCTRNYIH 180

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FF EF-618291-A. (Figgs b)

PD 67-027-1994 102757.

PR 27-1994 102757.

PR 27-1995 19-19-19146.

PR 27-1995 19-19-19146.

PR 27-1995 19-19-19146.

PR 27-1995 19-19-19141.

PR 27-19-1914 19-19141.

PR 27-1914 19-1914.

PR 27-1914 1 

Query Match Best Local Similarity 100.0%; Matches 9; Conservative

191 lfvofmlra 199

183 LFVSFMLRA 191

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Score 9; DB 12; Length 467; Pred. No. 6.19e-02; 0; Mismatches 0; Indels 0;

AC 84.1877 standard; Protein; 463 AA.

AC 84.1877; Set 18.187; Set 

Page 46

US-08-468-011A-2.rag

Tue Nov 24 08:10:58 1998

Page 45

Query Match 17%; Score 9; DB 8; Length 463; Best Local Similarity 100.0%; Pred. No. 6.19e-02; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

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PR F-518291-A. /label\* inserted maino acida
PD 05-077-1994.
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PD 05-077-1994.
PD 07-078-1995.
PR 07-1995.
PR RESULT 27

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Page 48

172 lhctrnyth 180 ||||||||||||| 172 LHCTRNYTH 180

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Princis were generated, based on the sequence flanking the Insertion forms in the bowns and rat sequence, and used to applify the forms in the bowns and rat sequence, and used to applify the forms of the property of the pr 888888888888

Score 9; DB 12; Length 475; Pred. No. 6.19e-02; 0; Mismatches 0; Indels 0; Gaps Query Match Best Local Similarity 100.0%; Matches 9; Conservative

172 lfvsfmlra 180 | | | | | | | | | | | | 183 LFVSFMLRA 191

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ö Query Match
1.7%; Score 9; DB 12; Length 476;
Bast Local Similarity 100.0%; Pred. No. 6.18-0.9;
Matches 9; Conservative 0; Mismatches 0; Indela

172 lfvsfmlra 180 ||||||||||| |183 LFVSFMLRA 191

RESULT 30 ID RS8671 standard; Protein; 476 AA. AC R58671; DT 12-MAY-1995 (first entry)

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955DB: 072203.

PR 24-JUN-1999; JP-183963.

PR 27-DEC-1999; JP-2831813.

PR 27-DEC-1999; JP-2831813.

PR 27-DEC-1999; JP-2831813.

PR 27-DEC-1999; JP-2831813.

PR 27-DEC-1999; JP-2831814.

PR 27-DEC-1999; JP-2831814.

PR 27-DEC-1999; JP-2831814.

PR 27-DEC-1999; JP-284184.

PR 27-DEC-1999; JP-284184.

PR 27-DEC-1999; JP-284184.

PR 27-DEC-1999; JP-284184.

CC This is the annion coid sequence, lacking the signal peptide sequence, of the human piculatary dedaylate crylase activitating polypeptide (RACAP).

CC This is the annion coid sequence, lacking the signal peptide sequence, of the human piculatary dedaylate crylase activitating polypeptide (RACAP).

CC This is the annion coid sequence, lacking the signal piculatary designate conditions of the membrane. This gene differs from the type 1-N gene by a 90 bp insertion between pastitions 121-1890. This snockes a procein containing through a calculated than the type 1-N gene by a 90 bp insertion between pastitions 121-1890. This encodes a procein containing the companion of the procein contains and the branch containing the type 1-B gene was called great by Procein in the bowine sequence of the puritied bowine because a deduced from the translate aver elecombined with a sequence flanking the insertion points in the bowine and rate sequences, and used to amplify the insertion points in the bowine and rate sequences, and used to amplify the insertion points in the bowine and rate sequences, and used to amplify the insertion points in the bowine and rate sequences, and used to amplify the insertion points in the bowine and rate sequences, and used to amplify the insertion points in the bowine and rate sequences, and used to amplify the insertion points in the bowine and rate sequences, and used to amplify the insertion points in the bowine and rate sequences, and used to amplify the selection who was a condition of a transmiss thereof a

Page 51

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Manna PACAP receptor type I canture procefu.

Bowine: ract, pituitary ademylate orginas activating polypeptide: DACAP;

Bowine: ract, pituitary ademylate orginas activating polypeptide: DACAP;

Bowine: pituitary;

Adaposis, raceptor;

Adaposis, raceptory

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Loanton/Qualifiers

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Page 52

Page 50

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proteins - used to develop prode. for use in the disgnosis and terminate neuroparty such an Althentar a dissense the remarker and the control of the control

Query Match
1.7%, Score 9; DB 12; Length 476;
Best Local Similarity 100,0%; pred. No. 6,199-02;
Matches 9; Conservative 0; Hismatches 0; Indels

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RESULT 39
ID RSSGES standard: Protein; 476 AA.

AC RSSGS:
D 12-MAY-1995 (first entry)
DE HUMAN PACAP.

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DE HUMAN PACAP.
RESULT STANDARD (first entry)
DE HUMAN PACAP.
RESULT STANDARD (cluster)
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Page 53

receptor can be used for gene therapy. Compounds isolated using screening assay can be used for treating neuropathy. Sequence 476 AA: ខូខូខូ

Ö Gaps Score 9; DB 12; Length 476; Pred. No. 6.19e-02; 0; Mismatches 0; Indels 0uery Match Best Local Similarity 100.0%; Matches 9; Conservative

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Best Local Similarity 100.0%; Pred. No. 6.18e-02;
Matches 9; Conservative 0; Mismatches 0; Indela

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172 lfvefmlra 180 |||||||||||||| 183 LFVSFMLRA 191

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NESULT 13 Reservant Protein; 485 AM.

IN Reservant Reservant Protein; 485 AM.

IN Reservant Rese

The rat receptor comprises 8 clusters of hydrophobic amino acida correspon to an N-terminal signal sequence and seven transmembrane domains 4 potential N-1, hard glycosylation sequence 485 AM;

Query March 1.7%; Score 9, DB 10; Length 485; Dest Local Similarity 100.0%; Pred No. 6.19-02; Indels 0; Caps Marches 9; Connervative 0; Minmatches 9; Connervative 0; Minmatches 9

170 lhetrnyth 178 ||||||||| 172 LHCTRNYIH 180 ò

Tue Nov 24 08:10:58 1998 Page 55

Query Match
1.74; Score 9; DB 12; Length 485;
Best Local Similarity 100.04; Pred. No. 6.196-02;
Manches 9; Conservative 0; Mismatches 0; Indels 0;

209 lfvsfmlra 217 ||||||||||| |183 LFVSFMLRA 191

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RESULT.

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Page 57

US-08-468-011A-2.rag

Tue Nov 24 08:10:58 1998

```
Bovine PACAP receptor type 1A protein.

Bovine; pituitary adonylate cyclase activating polypeptide; PACAP;

adonylate cyclase; receptor; type Al, signal sequence;

adonylate cyclase; receptor; type Al, signal sequence;

gland-derived; diagnosis; neuropathy; Alzheimer's disease; gene therapy;

accening; assay; neuropathy.
  /label= signal peptide
38..513
/label= mature peptide
  Location/Qualifiers
   Key
peptide
  peptide
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PR 25-FEB-1993; JP-03875.

PR 05-ARP 1993; JP-03875.

PR 27-ARP 1993; JP-03876.

PR 12-MEN 1993; JP-03889.

PR 27-MEN 1993; JP-03889.

PR 12-MEN 1994; JP-03889.

PR 12-MEN 1995; JP-03889.

PR 12-MEN 1995; JP-03889.

PR 12-MEN 1994; JP-03889.

PR 12-MEN 1995; JP-03889.

PR 12-MEN 1996; JP-03

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191 lfvsfmlra 199

g ð RESULT 35 ID RS6555 standard; Protein; 513 AA. AC R58655; DT 10-MAY-1995 (first entry)

Gaps ö Query Match 1.7%; Score 9; DB 12; Length 513; Best Local Similarity 100.0%; Pred. No. 6.13e-02; Matches 9; Conservative 0; Mismatches 0; Indels

Tue Nov 24 08:10:58 1998 Page 59

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anished prssst... is account of the human gene were deduced, based on the falliding his the rate and booken scotchem contains as by phosertion in the way lake the rate and booken scotchem contains as by phosertion in the sequences. And used to making the insertion points in the booking and release and anyelation inclei. The resultant products were recombined with the type lA gene to produced the subtypes called type 1B (672209). 1-33 (672209) and 1-C (67210). The subtypes are thought to arise by alternative splicing of a transcription product from a common gene. The ACAP, recorptor or fragments thereof may be used for the diagnosis of neuropathy such as Altheirar's disease. The DAM encoding the PACAP recorpors are also and alternative splicing assay computed as altheirary scotching assay can be used for treating neuropathy. 8888888888888888

Query Match 1.7%; Score 9; DB 13; Length 525; Best Local Similarity 100,0%; Pred. No. 6.19e-02; Matches 9; Conservative 0; Mismatches 0; Indels

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249 lfvsfmlra 257 ||||||||||||| 183 LFVSFMLRA 191

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PF FF-618791-A.

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IL MAY 1995 (first entry)

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Location/Qualifiers

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   Il SANC-1955 (Liter antrol 1) protein and the Calcar activating polypeptide: PACAP: Resentor type 13 protein and the Calcar activating polypeptide: PACAP: Manner activating polypeptide: PACAP: Administration of Calcar acceptor; type 1A; signal sequence; pituitary administration of Calcar activates; transmembrane; human, ACAP receptor; pituitary; pland-decired; diagnosis; neuropathy; Alabelmer's disease; gene therapy; signo satisfy assay; neuropathy; Alabelmer's disease; gene therapy; signo satisfy that the Calcar activation and the Calcar activation and the Calcar activation and the Calcar activation activation and the Calcar activation activation and the Calcar activation 
   1 BP - CARDAN - / JABORT - INDETTED FEBTON CO-CCT - 199. A CT - 19
  /label signal peptide 78.553 /label mature peptide 407.436 /label inserted region
                 158660 standard; Protein; 553 AA. (158660;
   peptide
   peptide
   domain
  PR 27-DEC-1999; JP-131175.

PR 17-DEC-1999; TAREAD CHEN TO LID.

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Page 63

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Page 64

Onery Match 1.7%; Score 9; DB 12; Length 553; Best Local Similarity 100(0%; Pred. No. 6.196-02; Matches 9; Conservative 0; Mismatches 0; Indels Matches 19; Conservative 0; Mismatches 0; Indels 249 lfvsfmlra 257 ||||||||||||| 183 LFVSFMLRA 191 g

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RESULT. 40
DR PA7714, standard; peptide; 10 AA.
AC PA7714, standard; peptide; 10 AA.
DE PHYPTISP Ecceptor fragment.
NR Parathypoid hormone; related protein; calcium; antegonist;
NR Parathypoid hormone; related protein; calcium; antegonist;
NR parathodise; hypercalcaemis; intracellular domain.
S synthetic.

Page 62

Page 61

US-08-468-011A-2.rag

1.7%; Score 9, DB 12; Length 552;
Best Local Similarity 100 0%; Pred. No. 6,19e-03; Indels 0; Gape Matches 9; Conservative 0; Mismatches 0; Indels 0; Gape

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based on the acquence flanking the insertion points in the bovine and rat sequence, and used to amplify the intervening region in huma pituliary and an angabated nuclei. The remittant products were ecombined with the type in graph of the produced the abbryges and left type is (072039), 1-52 (07209) and 1-c (07210). The abbryges and the type is (07209), 1-52 and 1-c (07210). The abbryges are thought to arise by Roche respons to Themperipal product from a common gene. The Roche respons to Themperipal product from a common gene. The receptor or fagments thereof may be used for the dispussal receptor can be used for gene the approach and a fall the party with a comparing the party may be used for gene therapy. Compounds labsard using the party may be used for treating neuropathy. 8888888888

Ouery Match 1.7%; Score 9; DB 12; Length 553; Dest Local Similarity 10ve, Pred. No. 6:19e-02; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

249 lfvofmlra 257 |||||||||| 183 LFVSFMLRA 191 g

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PF M00534631-A2.

Albela C terminal_intracellular_domain

DD 21-DEC-1995.

Al-THU-1995; U07757.

R 14-7UH-1995; U07757.

R 14-7UH-1995.

R 14-7UH-1995; U07757.

R 14-7UH-1995
  Query Match 1.5%; Score 8; DB 15; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.198+00;
Matches 8; Conservative 0; Mismatches 0. Indels 0; Gaps
      US-08-468-011A-2.rag
  /label~ Transmembrane_domain
364..411
/label~ C-terminal_intracellular_domain
Tue Nov 24 08:10:58 1998
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Page 69

/// /label= Phosphorylation site /note= "casein Kinase II phosphorylation site" 302 /label\* Phosphorylation\_site /note\* 'protein Kinase A phosphorylation site' 386 //label= Phosphorylation site //note= 'protein kinase C phosphorylation site'

modified\_site

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/label= Phosphorylation\_site //note= "protein Kinase C phosphorylation site" 222 /label= Phosphorylation\_site //note= 'protein kinase C phosphorylation site'

/label N-glycosylation\_site /label= N-glycosylation\_site 98

> modified\_site modified\_site

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Page 71
   RESULT 46
ID 897392 standard; Protein; 415 AA.
AC 897392 standard; Protein; 415 AA.
AC 897392 standard; Protein; 415 AA.
DI 21.ACU-1996 (Irat entry)
DE ACC 199792 STAND RESULT 45
ID REPORT

AC REPORT

AC REPRORMED Standard; Protein: 415 AA.

BY 7720.196 (first entry)
DE Mann CRP receptor CRP-RY.

BY Corticotopin releasing factor receptor; CRP-R; corticotiberin;
KN Gordinotopin CRP-RESULT CRP-RESULT CRP-R; corticotiberin;
FY GORDINOTOPIN CRP-RESULT CRP-RESULT CRP-RESULT CRP-R; corticotiberin;
FY GORDINOTOPIN CRP-RESULT CRP-RESU
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403 SFGGFFVS 410
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Page 72

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Onery Match 1.5% score 8 DB 17; Length 415; Bat Local Similarity 100 0% Pred. No. 1.138-40; Indels Matches 5; Conservative 0; Mismatches 0; Indels

PR WOSG19314.A. (Note= Protein Kinase C phosphorylation site\*)

PR WOSG19314.A. (Note= Protein Kinase C phosphorylation site\*)

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21.-WR.1993. UG-1026.

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23.-WR.1993. UG-1026.

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24.-WR.1993. UG-1026.

25.-WR.1993. UG-1026.

26.-WR.1993. UG-1026.

27.-WR.1993. UG-1026.

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28.-WR.1993. UG-1026.

28.-WR.1993. UG-1026.

29.-WR.1993. 
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Pituitary, homomer corticotropin releasing factor receptor:
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/note 'casein-kinase-II phosphorylation site'
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/note 'protein-kinase-A phosphorylation site'
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.7 47 869519, atandard, Protein, 415 AA. R69519, 21-AUG-1995 (first entry)

RESULT ID R69 AC R69 DT 21

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Page 76
    Page 74
   AC R69521;
DI 21-VOC-1905 (first entry)
DI 21
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   Gaps
   RESULT 59 and and and Protein: 415 Ah.

DE 187934 (first entry)

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Northcotrophi releasing factor receptor: CRF-R; corticoliberin;

NM angal. transduction.

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  Query Match 1.5%; Score 8; DB 13; Length 415; Best Local Similarity 100; 0%; Perel No. 1196+00; Marches 8; Conservative 0; Mismatches 0; Indels 0;
   US-08-468-011A-2.rag
  Search completed: Mon Nov 23 13:38:24 1998
Job time : 143 secs.
   353 sfqgffvs 360
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403 SFQCPPVS 410
    Tue Nov 24 08:10:58 1998
   Tue Nov 24 08:10:58 1998
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   Page 75
    Page 73
  RESULT 48

WO0159 stendard; Protein; 415 AM.

WO0159 (first entry)

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RW Human Conticotroph releasing factor receptor protein.

RW Human Conticotroph releasing factor receptor protein.

RW Human Suppression wettre ph. NCO2; sgoulst; entragonist; blood pressure;

RW Human Suppression.

PR 2-NUW-1994: DP-287638.

PR 22-NUW-1994: DP-287638.

PR COLUMN-1994: DP-287648.

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   PF W09617934.A.

PD 13-TM-1996.

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PD 13-TM-1996.

PR 09-DE-1994 (10-15353)

PR 09-DE-1995 (10-15353)

PR 09-DE
  Score 8; DB 17; Length 415;
Pred. No. 1.19e+00;
0; Mismatches 0; Indels 0; Gaps
   US-08-468-011A-2.rag
    US-08-468-011A-2.rag
  Odery Match 1.5%; Score 8; DB 18; Length 415; Best Local Similarity 100,0%; Pred. No. 1.19e-00; Matches 8; Conservative 0; Mismatches 0; Indels Matches 9; Conservative 0; Mismatches 0; Indels
  Score 8; DB 13; Length 415;
Pred. No. 1.19e+00;
0; Mismatches 0; Indels
  /label N-glycosylation_site
  /label- N-glycosylation_site
   //label N-glycosylation_site
  RESULT 49
ID R69521 standard; Protein; 415 AA.
  Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative
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Matches 8; Conservative
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| Page 21                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Page 23                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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REFERENCE AUTHORS TITLE

Contact: Robert Grausberg, Ph.D. 171; (0)) 496-1550 and Shalls Robert, Strausbergefulh, gov Films and Shalls Robert, Strausbergefulh, gov for through LiML; contact the This actions is available royalty-free through LiML; contact the This Contactium (infodinage, Lin), gov) for further information.

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Centre Hinton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uX Vector: pBiteeript II KS Vettor: pBiteeript II KS VETTOR: KS PBITEER: KS PBITEER: KS One pass dye-terminator sequencing of cosmid cloned genomic COMMENT

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Genomics 50 (1), 44-52 (1998) REFERENCE AUTHORS JOURNAL MEDLINE COMMENT TITLE

oncology Research Laboratories
Occology Research Laboratories
CRCS-424 57 Roginal Legistry St., Toronto, Ontario MSG 2M1, Canada
11-145 1401453
Fax: 415 1401453
Enail: I-hawleyfutoronto.ca

Page 27

BASE COUNT ORIGIN

Query Match 0.91; Score 19: DB 18: Length 220; Best Local Similarity 100.04; Pred No. 1.74e-05. Watches 19; Conservative 0; Mismatches 0; Indels 0;

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Homo.

Adams, M.D. Soares, M.D., Kerlavage, A.R., Fielda, C. and Venter, J.C.

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Page 26

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Trace considered overall poor quality Seq primer: -40ml3 ffwd. ET from Amersham Righ quality sequence stop: 1. Location/Qualifiers

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Best Local Similarity 100;04; Pred 18: 02.356-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

Db 459 GGGTTTGGCCAGGAGCAG 478 Cp 162 GGCTCTGGCCAGGAGGCAG 143

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Page 28

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| Page 33                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Peg 35                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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Possible reversed clone; polyT not found
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Romo sapiens Bukaryotae; mitochondrial eukaryotes; Metasoa; Chordata; Vertebrate; Hammalia; Butheria; Primates; Catarrhini; Hominidae; AA338897 297 bp mRNA EST 21-APR-1997 EST49310 Fetal brain I Homo sapiens CDNA 5' end, mRNA sequence AA338897 9199135 KEYWORDS SOURCE ORGANISM

1 (bases 1 to 297)
Adams, W.D., Soares, W.B., Rerlavage, A.R., Fields, C. and Venter, J.C.
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Page 40

Tue Nov 24 08:10:58 1998

Page 39

US-08-468-011A-1.rst

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Tue Nov 24 08:10:58 1998

Page 37

Page 38

1. (bease 1 to 2) Altureni, 7., Numera, Y. and Tauchiya, M. PRGS 502 Ret overlan CDNA primed with PRSS for 3 hours nombulished (1996)
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Mormaliation and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
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Tel: 314 266 1800
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  information related to this EST, please check the TiGR Human Gene
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928578 EST; CDNA sequence; putatively transcribed partial sequence; human.

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AA317471 314 bp mRNA BET 21-APR-1997 SPT 27-APR-1997 SPT 271239 Endometrial tumor Homo sapiens cDNA 5' end similar to spermidine/spermine NL-acetyltransferase, mRNA sequence. 45137471 SPT 27137471

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Initial seasement of human gene diversity and expression patterns bread upsylong 30 million, p. 37 e47 suppl.), 3-174 (1995) REFERENCE AUTHORS

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Occident: Pobert Strumberg, Ph.D. D. Tell; (301) 496-1550 Embergin, Ph.D. D. Emall: Robert Estrumberginh, post Tidoue Procurement: L. Jeffrey Medetroe, M.D., Michael R. Emart's Bott, M.D., Ph. Deffrey Medetroe, M.D., M. Deffrey Medetroe, M.D., M. Deffrey Medetroe, J. Deffrey Medetroe, J. Deffrey Medetroe, J. Deffrey Preparation: Strategene, Inc.

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Ridman, M. D., Rounaley, S.D., Field, C.E., Basa, S., Linher, K., Golden, K., Berry, K., Cranger, D., Suh, E., Wible, C., Shisuya, H., Simon, M. and Venter, J.C.

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Contect: Mark Adams
Department of Eukaryoric Genomics
Department of Eukaryoric Genomics
Department of Eukaryoric Genomics
Tex: 301 538 2030

Exail maddament of Contect Proma Research Genetics (info@tesgen.com). BAC

end search page 97742b/humgen/bac\_end\_search/bac\_end\_search.html.

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Page 60

West. Comparations of the process of the property of the process o R02745 421 bp mRNA EST Yer5600.rl Homo sapiens cDNA clone 123665 5'. R02745 9752481 RESULT 35
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Page 62

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Page 66

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Eukaryottes Aiveolatu; Apicomplexa; Coccidia; Elmeriida;
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WashO-Mercy Project
Mashington University School of Medicine
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   Contact: Robert Strausberg, Ph.D.
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## Tel: 314 286 1800 CMAIL: Cooperation.vustl.edu CMAIL: Cooperation.vustl.edu CMAIL: Cooperation.vustl.edu (1000es are available from Coome Systems (Genome600.NET); the (1000es are available from Coome Systems (Genome600.NET); the (1000es are available from Cooperation Cooperat RESULT 41 AA012966 415 bp MRNA EST 22-AUG-1996 LECTS 14.5 Mus musculus cDRNA ACESSION AA013968 5', MRNA sequence. AA012969 91504359 Ouery Match 0.94; Score 18; DB 9; Length 432; Best Local Similarity 10.04; Pred, No. 1.03-0.05 Matches 18; Conservative 0; Minmatches 0; Indels 0; Gaps US-08-468-011A-1.rst Tue Nov 24 08:10:58 1998

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Page 72 A EST 20-AUG-1996 Id tumor NDHPA Homo sapiens cDNA clone 1209 B61209 hypertension-induced protein /organism="Romo sapiens"
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/note="Organ: parathyroid gland; Vector: p7773D
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Still and Cancer Institute, Cancer Genome Anatomy Project (GGAP),
Thusor Gene index
   Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
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Brodentia, Sciurognathi, Muridae, Murinae; Mus.

Brodentia, Sciurognathi, Muridae, Murinae; Mus.

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Page 79

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Wilson, R. The WashU-Merck EST Project Unpublished (1995)

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